

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
19 December 2002 (19.12.2002)

PCT

(10) International Publication Number
WO 02/101075 A2

(51) International Patent Classification⁷: **C12Q**

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(21) International Application Number: PCT/US02/18638

(22) International Filing Date: 12 June 2002 (12.06.2002)

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(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(26) Publication Language: English

(30) Priority Data:
60/298,159 13 June 2001 (13.06.2001) US
60/298,155 13 June 2001 (13.06.2001) US
60/335,936 14 November 2001 (14.11.2001) US

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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

(57) Abstract: The invention relates to newly discovered nucleic acid molecules and proteins associated with cervical cancer including pre-malignant conditions such as dysplasia. Compositions, kits, and methods for detecting, characterizing, preventing, and treating human cervical cancers are provided.

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NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
CERVICAL CANCER

5 RELATED APPLICATIONS

The present application claims priority to U.S. provisional patent application serial no. 60/298,159, filed on June 13, 2001, U.S. provisional patent application serial no. 60/298,155, filed on June 13, 2001, and U.S. provisional patent application serial no. 60/335,936, filed on November 14, 2001, all of which are expressly incorporated by
10 reference.

FIELD OF THE INVENTION

The field of the invention is cervical cancer, including diagnosis, characterization, management, and therapy of cervical cancer.

15

BACKGROUND OF THE INVENTION

The increased number of cancer cases reported in the United States, and, indeed, around the world, is a major concern. Currently there are only a handful of treatments available for specific types of cancer, and these provide no absolute guarantee
20 of success. In order to be most effective, these treatments require not only an early detection of the malignancy, but a reliable assessment of the severity of the malignancy.

Cancer of the cervix is one of the most common malignancies in women and remains a significant public health problem throughout the world. In the United States alone, invasive cervical cancer accounts for approximately 19% of all
25 gynecological cancers. In 1996, it was estimated that there were 14,700 newly diagnosed cases and 4900 deaths attributed to this disease (American Cancer Society, Cancer Facts & Figures 1996, Atlanta, Ga.: American Cancer Society, 1996). In many developing countries, where mass screening programs are not widely available, the clinical problem is more serious. Worldwide, the number of new cases is estimated to be 471,000 with a
30 four-year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer* In: "Human Papillomavirus", New York, Oxford Press, pp 9-39; National Institutes of Health, Consensus Development Conference Statement on Cervical Cancer, Apr.1-3, 1996).

The precursor to cervical cancer is dysplasia, also known in the art as cervical intraepithelial neoplasia (CIN) or squamous intraepithelial lesions (SIL). While it is not understood how normal cells become transformed, the concept of a continuous spectrum of histopathological change from normal, stratified epithelium through CIN to
5 invasive cancer has been widely accepted for many years. A large body of epidemiological and molecular biological evidence has established human papillomavirus (HPV) infection as a causative factor in cervical cancer. HPV is found in 85% or more of squamous cell invasive lesions, which represent the most common histologic type seen in cervical carcinoma. Additional cofactors have also been
10 identified, including oncogenes that have been activated by point mutations and chromosomal translocations or deletions.

In light of this, cervical cancer remains a highly preventable form of cancer when pre-invasive lesions are detected early. Cytological examination of Papanicolaou-stained cervical smears (also referred to as Pap smears) is currently the
15 principle method for detecting cervical cancer. Not surprisingly, the effectiveness of Pap smear screening varies depending not only upon the quality of the sample being used, but also upon subjective parameters that are inherent to the analysis. In addition, despite the historical success of the test, concerns have arisen regarding its ability to reliably predict the behavior of some pre-invasive lesions (Ostor *et al.*, 1993, *Int. J. Gynecol.*
20 *Pathol.* 12: 186-192; and Genest *et al.*, 1993, *Human Pathol.* 24: 730-736).

SUMMARY OF THE INVENTION

The invention relates to cancer markers (hereinafter "markers" or "markers of the inventions"), which are listed in Table 1. The invention provides
25 nucleic acids and proteins that are encoded by or correspond to the markers (hereinafter "marker nucleic acids" and "marker proteins," respectively). Table 1 provides the sequence identifiers of the sequences of such marker nucleic acids and proteins listed in the accompanying Sequence Listing. The invention further provides antibodies, antibody derivatives and antibody fragments which bind specifically with such proteins
30 and/or fragments of the proteins.

The invention also relates to various methods, reagents and kits for diagnosing, staging, prognosing, monitoring and treating cervical cancer. "Cervical cancer" as used herein includes carcinomas, (*e.g.*, carcinoma in situ, invasive

carcinoma, metastatic carcinoma) and pre-malignant conditions, (*e.g.*, dysplasia, including CIN or SIL). In one embodiment, the invention provides a diagnostic method of assessing whether a patient has cervical cancer or has higher than normal risk for developing cervical cancer, comprising the steps of comparing the level of expression of
5 a marker of the invention in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a sample from a patient without cervical cancer. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer or has higher than normal risk for developing cervical cancer.

10 According to the invention, the markers are selected such that the positive predictive value of the methods of the invention is at least about 10%, preferably about 25%, more preferably about 50% and most preferably about 90%. Also preferred for use in the methods of the invention are markers that are differentially expressed, as compared to normal cervical cells, by at least two-fold in at least about 20%, more
15 preferably about 50% and most preferably about 75% of any of the following conditions: stage 0 cervical cancer patients, stage I cervical cancer patients, stage II cervical cancer patients, stage III cervical cancer patients, stage IV cervical cancer patients, grade I cervical cancer patients, grade II cervical cancer patients, grade III cervical cancer patients, squamous cell (epidermoid) cervical cancer patients, cervical adenocarcinoma
20 patients, cervical adenosquamous carcinoma patients, small-cell cervical carcinoma patients, malignant cervical cancer patients, patients with primary carcinomas of the cervix, patients with primary malignant lymphomas of the cervix and patients with secondary malignant lymphomas of the cervix, and all other types of cancers, malignancies and transformations associated with the cervix.

25 In a preferred diagnostic method of assessing whether a patient is afflicted with cervical cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:
a) the level of expression of a marker of the invention in a patient sample,
and
30 b) the normal level of expression of the marker in a control non-cervical cancer sample.

A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

The invention also provides diagnostic methods for assessing the efficacy
5 of a therapy for inhibiting cervical cancer in a patient. Such methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, and
- 10 b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the therapy is efficacious for inhibiting cervical cancer in the patient.

15 It will be appreciated that in these methods the "therapy" may be any therapy for treating cervical cancer including, but not limited to, chemotherapy, radiation therapy, surgical removal of tumor tissue, gene therapy and biologic therapy such as the administering of antibodies and chemokines. Thus, the methods of the invention may be used to evaluate a patient before, during and after therapy, for
20 example, to evaluate the reduction in tumor burden.

In a preferred embodiment, the diagnostic methods are directed to therapy using a chemical or biologic agent. These methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient and maintained in the presence of the chemical or biologic
25 agent, and
- b) expression of the marker in a second sample obtained from the patient and maintained in the absence of the agent.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the agent is efficacious for inhibiting cervical
30 cancer, in the patient. In one embodiment, the first and second samples can be portions of a single sample obtained from the patient or portions of pooled samples obtained from the patient.

The invention additionally provides a monitoring method for assessing the progression of cervical cancer in a patient, the method comprising:

- a) detecting in a patient sample at a first time point, the expression of a marker of the invention;
- 5 b) repeating step a) at a subsequent time point in time; and
- c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer in the patient.

A significantly higher level of expression of the marker in the sample at the subsequent time point from that of the sample at the first time point is an indication that the cervical cancer has progressed, whereas a significantly lower level of expression is an indication
10 that the cervical cancer has regressed.

The invention further provides a diagnostic method for determining whether cervical cancer has metastasized or is likely to metastasize in the future, the method comprising comparing:

- 15 a) the level of expression of a marker of the invention in a patient sample, and
- b) the normal level (or non-metastatic level) of expression of the marker in a control sample.

A significantly higher level of expression in the patient sample as compared to the
20 normal level (or non-metastatic level) is an indication that the cervical cancer has metastasized or is likely to metastasize in the future.

The invention moreover provides a test method for selecting a composition for inhibiting cervical cancer in a patient. This method comprises the steps of:

- 25 a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker of the invention in each of the aliquots; and
- 30 d) selecting one of the test compositions which significantly reduces the level of expression of the marker in the aliquot containing that test composition, relative to the levels of expression of the marker in the presence of the other test compositions.

The invention additionally provides a test method of assessing the cervical carcinogenic potential of a compound. This method comprises the steps of:

- a) maintaining separate aliquots of cervical cells in the presence and absence of the compound; and
- 5 b) comparing expression of a marker of the invention in each of the aliquots.

A significantly higher level of expression of the marker in the aliquot maintained in the presence of the compound, relative to that of the aliquot maintained in the absence of the compound, is an indication that the compound possesses cervical carcinogenic potential.

10 In addition, the invention further provides a method of inhibiting cervical cancer in a patient. This method comprises the steps of:

- a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of compositions;
- 15 c) comparing expression of a marker of the invention in each of the aliquots; and
- d) administering to the patient at least one of the compositions which significantly lowers the level of expression of the marker in the aliquot containing that composition, relative to the levels of expression of the marker in the presence of the other compositions.

20 In the aforementioned methods, the samples or patient samples comprise cells obtained from the patient. The cells may be found in a cervical smear collected, for example, by a cervical brush. In another embodiment, the sample is a body fluid. Such fluids include, for example, blood fluids, lymph, ascitic fluids, gynecological fluids, urine, and fluids collected by vaginal rinsing. In a further embodiment, the patient sample is *in vivo*.

According to the invention, the level of expression of a marker of the invention in a sample can be assessed, for example, by detecting the presence in the sample of:

- 30 • the corresponding marker protein (*e.g.*, a protein having one of the sequences set forth as "SEQ ID NO (AAs)" in Table 1, or a fragment of the protein (*e.g.* by using a reagent, such as an antibody, an antibody derivative,

an antibody fragment or single-chain antibody, which binds specifically with the protein or protein fragment)

- the corresponding marker nucleic acid (*e.g.* a nucleotide transcript having one of the nucleic acid sequences set forth as “SEQ ID NO (nts)” in Table 1, or a complement thereof), or a fragment of the nucleic acid (*e.g.* by contacting transcribed polynucleotides obtained from the sample with a substrate having affixed thereto one or more nucleic acids having the entire or a segment of the nucleic acid sequence of any of the SEQ ID NO (nts), or a complement thereof)
- a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by the corresponding marker protein.

According to the invention, any of the aforementioned methods may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of cervical cancer markers, including cervical cancer markers known in the art. In such methods, the level of expression in the sample of each of a plurality of markers, at least one of which is a marker of the invention, is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer. A significantly altered (*i.e.*, increased or decreased as specified in the above-described methods using a single marker) level of expression in the sample of one or more markers of the invention, or some combination thereof, relative to that marker's corresponding normal or control level, is an indication that the patient is afflicted with cervical cancer. For all of the aforementioned methods, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%.

In a further aspect, the invention provides an antibody, an antibody derivative, or an antibody fragment, which binds specifically with a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing) or a fragment of the protein. The invention also provides methods for making such antibody, antibody derivative, and antibody fragment. Such methods may comprise immunizing a mammal with a protein or peptide comprising the entirety, or a segment of 10 or more amino acids, of a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), wherein the protein or peptide may be obtained from a cell or by chemical synthesis. The methods of the invention also encompass producing

monoclonal and single-chain antibodies, which would further comprise isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for those that produce an antibody that binds specifically with a marker protein or a
5 fragment of the protein.

In another aspect, the invention relates to various diagnostic and test kits. In one embodiment, the invention provides a kit for assessing whether a patient is afflicted with cervical cancer. The kit comprises a reagent for assessing expression of a marker of the invention. In another embodiment, the invention provides a kit for
10 assessing the suitability of a chemical or biologic agent for inhibiting cervical cancer in a patient. Such a kit comprises a reagent for assessing expression of a marker of the invention, and may also comprise one or more of such agents. In a further embodiment, the invention provides kits for assessing the presence of cervical cancer cells or treating cervical cancers. Such kits comprise an antibody, an antibody derivative, or an antibody
15 fragment, which binds specifically with a marker protein, or a fragment of the protein. Such kits may also comprise a plurality of antibodies, antibody derivatives, or antibody fragments wherein the plurality of such antibody agents binds specifically with a marker protein, or a fragment of the protein.

In an additional embodiment, the invention also provides a kit for
20 assessing the presence of cervical cancer cells, wherein the kit comprises a nucleic acid probe that binds specifically with a marker nucleic acid or a fragment of the nucleic acid. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a marker nucleic acid, or a fragment of the nucleic acid.

In a further aspect, the invention relates to methods for treating a patient
25 afflicted with cervical cancer or at risk of developing cervical cancer. Such methods may comprise reducing the expression and/or interfering with the biological function of a marker of the invention. In one embodiment, the method comprises providing to the patient an antisense oligonucleotide or polynucleotide complementary to a marker nucleic acid, or a segment thereof. For example, an antisense polynucleotide may be
30 provided to the patient through the delivery of a vector that expresses an anti-sense polynucleotide of a marker nucleic acid or a fragment thereof. In another embodiment, the method comprises providing to the patient an antibody, an antibody derivative, or antibody fragment, which binds specifically with a marker protein or a fragment of the

protein. In a preferred embodiment, the antibody, antibody derivative or antibody fragment binds specifically with a protein having one of the amino acid sequences set forth in the Sequence Listing, or a fragment of the protein.

It will be appreciated that the methods and kits of the present invention may also include known cancer markers including known cervical cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than cervical cancer.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to newly discovered cancer markers associated with the cancerous state of cervical cells. It has been discovered that the higher than normal level of expression of any of these markers or combination of these markers correlates with the presence of cervical cancer including pre-malignant conditions such as dysplasia, in a patient. Methods are provided for detecting the presence of cervical cancer in a sample, the absence of cervical cancer in a sample, the stage of a cervical cancer, and other characteristics of cervical cancer that are relevant to prevention, diagnosis, characterization, and therapy of cervical cancer in a patient. Methods of treating cervical cancer are also provided.

Table 1 lists the markers of the invention which are over-expressed in cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells and comprises markers listed in Tables 2 and 3. Table 2 lists newly-identified nucleotide and amino acid sequences. Table 3 lists newly-identified nucleotide sequences. Tables 1-3 provide the sequence listing identifiers of the cDNA sequence of a nucleotide transcript and the amino acid sequence of a protein encoded by or corresponding to each marker, as well as the location of the protein coding sequence within the cDNA sequence.

Table 1

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..11946
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..11922
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..12000
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..11976
M1	APOL1: Apolipoprotein L-I mRNA, splice variant A, major form	9	10	213..1364
M2	APOL1: Apolipoprotein L-I mRNA, splice variant B, minor form	11	12	274..1518
M3	APOL3: apolipoprotein L, 3; TNF-inducible protein CG12-1	13	14	418..1413
OV3	AQP5: Aquaporin 5	15	16	519..1316
M4	BC001980: clone MGC:5618	17	18	157..225
M5	BST2: Bone marrow stromal cell antigen 2	19	20	10..552
M6	BTEB1: basic transcription element binding protein 1	21	22	1265..1999
M665	CD74: CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	23	24	8..706
M7	CDC20: CDC20 cell cycle protein	25	26	45..1544
M8	CDKN2C: cyclin-dependent kinase inhibitor 2C, p18	27	28	1216..1722
M9	CKTSF1B1: (cysteine knot superfamily 1, BMP antagonist 1), gremlin	29	30	45..1544
M10	CLDN1: claudin 1	31	32	221..856
M11	CLIC4: chloride intracellular channel 4	33	34	198..959
M12	COL1A1: collagen, type I, alpha 1	35	36	120..4514
M13	COL1A2: collagen, type I, alpha 2	37	38	140..4240
M14	COL8A1: collagen, type VIII, alpha 1	39	40	1..2235
M15	COPA: coatamer protein complex, subunit alpha	41	42	467..4141
M16	CRIP1: cysteine-rich protein 1 (intestinal)	43	44	1..234
M17	CTGF: connective tissue growth factor	45	46	146..1195
M18	DOC: downregulated in ovarian cancer 1	47	48	135..2393
M19	EFNA1: ephrin-A1	49	50	74..691
M481	EPPK1: epiplakin 1	51	52	89..15286
M20	FLJ11350: hypothetical protein FLJ11350	53	54	106..1047
M21	FLJ13809: hypothetical protein FLJ13809	55	56	64..1593
M22	FLJ20500: hypothetical protein FLJ20500	57	58	198..896
M23	FLJ23399: hypothetical protein FLJ23399	59	60	283..1770
M24	FN1: Fibronectin 1, variant 1	61	62	<1..2384
M25	FN1: Fibronectin 1, variant 2	63	64	<1..6988
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M26	FY: Duffy blood group	70	71	495..1511

M485	G1P3:interferon, alpha-inducible protein (clone IFI-6-16)	72	73	108..500
M486	GW112: GW112 protein	74	75	509..1072
M27	HSKERUV: clone 266, Human radiated keratinocyte mRNA 266 (keratin-related protein)	76	77	<1..801
M28	HSPC121: butyrate-induced transcript 1	78	79	150..1271
M29	HUMCLPB: Coactosin like protein	80	81	150..576
M487	hypothetical protein	82	83	58..8163
M30	IFI27: (interferon, alpha-inducible protein 27	84	85	55..423
OV31	IFI30: interferon, gamma-inducible protein 30	86	87	41..952
M31	IFITM2: interferon induced transmembrane protein 2 (1-8D)	88	89	280..678
M32	IGFBP-3: insulin-like growth factor binding protein 3	90	91	133..1009
M33	IL8RA: interleukin 8	92	93	75..374
M34	INHBA: Inhibin, beta-1	94	95	86..1366
M488	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant a	96	97	74..3229
M454	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant b	98	99	74..3274
M35	ITGB6: integrin, beta 6	100	101	195..2561
M36	KATII: L-kynurenine/alpha-aminoadipate aminotransferase	102	103	454..1731
M666	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 1	104	105	89..1315
M667	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 2	106	107	54..1313
M668	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 3	108	109	28..1233
M37	KIAA0662: KIAA0662 protein	110	111	<1..2035
M38	LAMA3: Laminin, alpha-3 (nicein (150kD), (kalinin (165kD), BM600 (150kD)	112	113	1..5142
M39	LAMC2: laminin, gamma 2	114	115	90..3671
M40	LSM5: U6 snRNA-associated Sm-like protein	116	117	1..276
M41	LUM: lumican	118	119	85..1101
M42	MACMARCKS: macrophage myristoylated alanine-rich C kinase substrate	120	121	14..601
M43	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 1	122	123	115..666
M44	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 2	124	125	100..651
M45	MAPK: mitogen-activated protein kinase 1	126	127	328..1410
M489	MCM6: minichromosome maintenance deficient (mis5, S. pombe) 6	128	129	62..2527
M46	MDK: midkine (neurite growth-promoting factor 2)	130	131	26..457
M47	MGP: matrix Gla protein	132	133	47..358
M48	MMP12: matrix metalloproteinase 12	134	135	13..1425
M49	MMP3: matrix metalloproteinase 3, stromelysin 1, progelatinase	136	137	64..1497
M294	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 1	138	139	48..851
OV52	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 2	140	139	28..831

M50	MMP9: matrix metalloproteinase 9, gelatinase B, 92kD gelatinase, 92kD type IV collagenase	141	142	20..2143
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
OV43	MSLN: mesothelin, variant 6	153	154	88..1956
OV45	MUC1: mucin 1, transmembrane, variant 1	155	156	58..1605
M669	MUC1: mucin 1, transmembrane, variant 2	157	158	74..3841
M51	MYBL2: v-myb avian myeloblastosis viral oncogene homolog-like 2	159	160	128..2230
M52	MYH11: smooth muscle myosin heavy chain 11, isoform SM1	161	162	89..6007
M53	MYH11: smooth muscle myosin heavy chain 11, isoform SM2	163	164	89..5905
M54	NK4: natural killer cell transcript 4, variant 1	165	166	60..764
M670	NK4: natural killer cell transcript 4, variant 2	167	168	60..764
M55	NP25: (neuronal protein)	169	170	50..898
OV48	OPN-a (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	171	172	1..942
OV49	OPN-b (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	173	174	88..990
OV50	OPN-c (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	175	176	1..861
M56	OSF-2, osteoblast specific factor 2 (fascin-like), variant 1	177	178	12..2522
M491	OSF-2, osteoblast specific factor 2 (fascin-like), variant 2	179	180	28..2367
M57	PIM2: pim-2 oncogene	181	182	186..1190
M58	PLAU: plasminogen activator, urokinase	183	184	77..1372
M59	PLK: polo (Drosophila)-like kinase	185	186	64..1875
M671	PNN: pinin, desmosome associated protein	187	188	31..2262
M60	PRG1: proteoglycan 1, secretory granule	189	190	25..501
M61	PTH1H: parathyroid hormone-like hormone	191	192	304..831
M62	PTN: pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	193	194	1542..2048
M63	RAB6KIFL: RAB6 interacting, kinesin-like (rabkinesin6)	195	196	28..2700
M64	RARRES3: retinoic acid receptor responder (tazarotene induced) 3	197	198	62..556
M65	RBP1: retinol-binding protein 1 (cellular), CRABP-I, CRBP-I	199	200	126..533
M66	RGS16: Regulator of G protein signaling-16	201	202	93..701
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
M68	S100A2: S100 calcium binding protein A2, variant 2	205	206	41..334
M69	SCYA20: small inducible cytokine subfamily A (Cys-Cys), member 20	207	208	59..349
M70	SPARC: Osteonectin (secreted protein, acidic, cysteine-rich)	209	210	58..969
M71	STCH: stress 70 protein chaperone, microsome-associated	211	212	37..1452
M492	STK12: serine/ threonine kinase 12	213	214	58..1092

M72	TK1: thymidine kinase 1, soluble	215	216	58..762
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M73	TMSB4X: thymosin, beta 4, X chromosome	219	220	78..212
M74	TOP2A: topoisomerase (DNA) II alpha (170kD)	221	222	37..4632
M493	TPM1: tropomyosin 1 (alpha)	223	224	57..911
M75	TXN: thioredoxin	225	226	64..381
M76	UBCH10: ubiquitin carrier protein E2-C	227	228	41..580
M77	UBD: diubiquitin	229	230	19..516
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508
M80	VATD: vacuolar proton pump delta polypeptide	235	236	166..909
M81	ZWINT: ZW10 interactor	237	238	25..858

Table 2

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..1194 6
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..1192 2
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..1200 0
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..1197 6
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
M670	NK4: natural killer cell transcript 4, variant 2	167	168	60..764
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508

Table 3

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M481	EPPK1: epiplakin 1	51	52	89..15286
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M35	ITGB6: integrin, beta 6	100	101	195..2561
OV43	MSLN: mesothelin, variant 6	153	154	88..1956

Definitions

5 As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

10 A "marker" is a gene whose altered level of expression in a tissue or cell from its expression level in normal or healthy tissue or cell is associated with a disease state, such as cancer. A "marker nucleic acid" is a nucleic acid (*e.g.*, mRNA, cDNA) encoded by or corresponding to a marker of the invention. Such marker nucleic acids include DNA (*e.g.*, cDNA) comprising the entire or a partial sequence of any of the
15 nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence. The marker nucleic acids also include RNA comprising the entire or a partial sequence of any of the nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence, wherein all thymidine residues are replaced with uridine residues. A "marker protein" is a protein encoded by or corresponding to a
20 marker of the invention. A marker protein comprises the entire or a partial sequence of any of the sequences set forth in the Sequence Listing. The terms "protein" and "polypeptide" are used interchangeably.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example, a nucleotide transcript or
25 protein encoded by or corresponding to a marker. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as

described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

A "cervical-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through cervical cells or into which cells or proteins shed from cervical cells are capable of passing. The cells may be found in a cervical smear collected, for example, by a cervical brush. Exemplary cervical-associated body fluids include blood fluids, lymph, ascitic fluids, gynecological fluids, cystic fluid, urine, and fluids collected by vaginal rinsing.

The "normal" level of expression of a marker is the level of expression of the marker in cervical cells of a human subject or patient not afflicted with cervical cancer

An "over-expression" or "significantly higher level of expression" of a marker refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least twice, and more preferably three, four, five or ten times the expression level of the marker in a control sample (*e.g.*, sample from a healthy subjects not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

A "significantly lower level of expression" of a marker refers to an expression level in a test sample that is at least twice, and more preferably three, four, five or ten times lower than the expression level of the marker in a control sample (*e.g.*, sample from a healthy subject not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

As used herein, the term "promoter/regulatory sequence" means a nucleic acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses the gene product in a tissue-specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

5 An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

10 A "tissue-specific" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

 A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.* an mRNA, hnRNA, a cDNA, or an analog of such RNA or cDNA) which is complementary to or homologous with all or a portion of a mature mRNA made by transcription of a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the RNA transcript, and reverse transcription of the RNA transcript.

 "Complementary" refers to the broad concept of sequence complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing

with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity
5 between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is
10 expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and
15 preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A molecule is "fixed" or "affixed" to a substrate if it is covalently or non-
20 covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.* standard saline citrate, pH 7.4) without a substantial fraction of the molecule dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in an organism found
25 in nature.

A cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, cervical cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (*e.g.* a package or container) comprising at least
30 one reagent, *e.g.* a probe, for specifically detecting the expression of a marker of the invention. The kit may be promoted, distributed, or sold as a unit for performing the methods of the present invention.

“Proteins of the invention” encompass marker proteins and their fragments; variant marker proteins and their fragments; peptides and polypeptides comprising an at least 15 amino acid segment of a marker or variant marker protein; and fusion proteins comprising a marker or variant marker protein, or an at least 15 amino acid segment of a marker or variant marker protein.

Unless otherwise specified herewithin, the terms “antibody” and “antibodies” broadly encompass naturally-occurring forms of antibodies (*e.g.*, IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody.

Description

The present invention is based, in part, on newly identified markers which are over-expressed in cervical cancer cells as compared to their expression in normal (*i.e.* non-cancerous) cervical cells. The enhanced expression of one or more of these markers in cervical cells is herein correlated with the cancerous state of the tissue. The invention provides compositions, kits, and methods for assessing the cancerous state of cervical cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells) as well as treating patients afflicted with cervical cancer.

The compositions, kits, and methods of the invention have the following uses, among others:

- 1) assessing whether a patient is afflicted with cervical cancer;
- 2) assessing the stage of cervical cancer in a human patient;
- 3) assessing the grade of cervical cancer in a patient;
- 4) assessing the benign or malignant nature of cervical cancer in a patient;
- 5) assessing the metastatic potential of cervical cancer in a patient;
- 6) assessing the histological type of neoplasm associated with cervical cancer in a patient;

- 7) making antibodies, antibody fragments or antibody derivatives that are useful for treating cervical cancer and/or assessing whether a patient is afflicted with cervical cancer;
- 8) assessing the presence of cervical cancer cells;
- 5 9) assessing the efficacy of one or more test compounds for inhibiting cervical cancer in a patient;
- 10 10) assessing the efficacy of a therapy for inhibiting cervical cancer in a patient;
- 11) monitoring the progression of cervical cancer in a patient;
- 10 12) selecting a composition or therapy for inhibiting cervical cancer in a patient;
- 13) treating a patient afflicted with cervical cancer;
- 14) inhibiting cervical cancer in a patient;
- 15 15) assessing the cervical carcinogenic potential of a test compound; and
- 16) preventing the onset of cervical cancer in a patient at risk for developing cervical cancer.

The invention thus includes a method of assessing whether a patient is afflicted with cervical cancer which includes assessing whether the patient has pre-
20 metastasized cervical cancer. This method comprises comparing the level of expression of a marker of the invention (listed in Table 1) in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a non-cervical cancer sample. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

25 Gene delivery vehicles, host cells and compositions (all described herein) containing nucleic acids comprising the entirety, or a segment of 15 or more nucleotides, of any of the nucleic acid sequences set forth in the Sequence Listing, or the complement of such sequences, and polypeptides comprising the entirety, or a segment of 10 or more amino acids, of any of the amino acid sequences set forth in the Sequence
30 Listing, are also provided by this invention.

As described herein, cervical cancer in patients is associated with an increased level of expression of one or more markers of the invention. While, as discussed above, some of these changes in expression level result from occurrence of the

cervical cancer, others of these changes induce, maintain, and promote the cancerous state of cervical cancer cells. Thus, cervical cancer characterized by an increase in the level of expression of one or more markers of the invention can be inhibited by reducing and/or interfering with the expression of the markers and/or function of the proteins encoded by those markers.

Expression of a marker of the invention can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be provided to the cervical cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment which specifically binds a marker protein, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein. The expression and/or function of a marker may also be inhibited by treating the cervical cancer cell with an antibody, antibody derivative or antibody fragment that specifically binds a marker protein. Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of a marker or inhibit the function of a marker protein. The compound so identified can be provided to the patient in order to inhibit cervical cancer cells of the patient.

Any marker or combination of markers of the invention, as well as any known markers in combination with the markers of the invention, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in cervical cancer cells and the level of expression of the same marker in normal cervical cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method, and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater than the level of expression of the same marker in normal cervical tissue.

It is recognized that certain marker proteins are secreted from cervical cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the such marker proteins can be detected in a cervical-associated body fluid sample, which may be more easily collected from a human patient than a tissue biopsy sample. In addition, preferred *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

It is a simple matter for the skilled artisan to determine whether any particular marker protein is a secreted protein. In order to make this determination, the marker protein is expressed in, for example, a mammalian cell, preferably a human cervical cell line, extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein. About 8×10^5 293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO₂, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424- 54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-³⁵S™ reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO₂ atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris.

The presence of the protein in the supernatant is an indication that the protein is secreted.

It will be appreciated that patient samples containing cervical cells may be used in the methods of the present invention. In these embodiments, the level of expression of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker in a cervical cell sample, *e.g.*, cervical smear obtained from a patient. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.*, nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the sample. Likewise, cervical smears may also be subjected to post-collection preparative and storage techniques, *e.g.*, fixation.

The compositions, kits, and methods of the invention can be used to detect expression of marker proteins having at least one portion which is displayed on the surface of cells which express it. It is a simple matter for the skilled artisan to determine whether a marker protein, or a portion thereof, is exposed on the cell surface. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker protein having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed nucleic acid or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

In a preferred embodiment, expression of a marker is assessed using an antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin}), or an

antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a marker protein or fragment thereof, including a marker protein which has undergone all or a portion of its normal post-translational modification.

5 In another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to
10 hybridization with the reference polynucleotide; preferably, it is not amplified. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker of the invention may be used to detect occurrence of a
15 marker in a patient.

 In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.* at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker nucleic
20 acid. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (*e.g.* detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (*e.g.* a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of
25 assessing marker expression is used which involves hybridization of one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

 Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it
30 is preferable that the level of expression of the marker is significantly greater than the minimum detection limit of the method used to assess expression in at least one of normal cervical cells and cancerous cervical cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over-expressed in cancers of various types, including specific cervical cancers, as well as other cancers such as breast cancer, ovarian cancer, etc. For example, it will be confirmed that some of the markers of the invention are over-expressed in most (*i.e.* 50% or more) or substantially all (*i.e.* 80% or more) of cervical cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with cervical cancer of various stages (*i.e.* stage 0, I, II, III, and IV cervical cancers, as well as subclassifications IA1, IA2, IB, IB1, IB2, IIA, IIB, IIIA, IIIB, IVA, and IVB, using the FIGO Stage Grouping system for primary carcinoma of the cervix (see *Gynecologic Oncology*, 1991, 41:199 and *Cancer*, 1992, 69:482)), and pre-malignant conditions (*e.g.*, dysplasia including CIN or SIL), of various histologic subtypes (*e.g.* squamous cell carcinomas and squamous cell carcinoma variants such as verrucous carcinoma, lymphoepithelioma-like carcinoma, papillary squamous neoplasm and spindle cell squamous cell carcinoma (see *Cervical Cancer and Preinvasive Neoplasia*, 1996, pp. 90-91) serous, mucinous, endometrioid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal {Müllerian} mixed tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant cervical tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue}). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in patients.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%,
5 and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with a cervical cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a positive predictive value (PPV) of greater than about 10% is obtained for the general population (more preferably coupled with an assay
10 specificity greater than 80%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single
15 reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly increased level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. When a plurality of markers
20 is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-cervical origin in a patient sample), it is preferable that the marker of the invention used therein be a
25 marker which has a restricted tissue distribution, *e.g.*, normally not expressed in a non-cervical tissue.

Only a small number of markers are known to be associated with cervical cancer (*e.g.* bcl-2, 15A8 antigen, cdc6, Mcm5, and EGFR). These markers are not, of course, included among the markers of the invention, although they may be used
30 together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the

invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

It is recognized that the compositions, kits, and methods of the invention
5 will be of particular utility to patients having an enhanced risk of developing cervical cancer and their medical advisors. Patients recognized as having an enhanced risk of developing cervical cancer include, for example, patients having a familial history of cervical cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients of advancing age (*i.e.* women older than about 50 or 60 years).

10 The level of expression of a marker in normal (*i.e.* non-cancerous) human cervical tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of cervical cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the cervical cells
15 which is suspected of being cancerous. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample
20 obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cervical cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the presence of cervical cancer cells in a sample (*e.g.* an archived tissue sample or a sample
25 obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a paraffinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the
30 kits of the invention, or the methods used to assess levels of marker expression in the sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of cervical cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a marker nucleic acid or protein. Suitable reagents for binding with a marker protein include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a marker nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal cervical cells, a sample of cervical cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether patient is afflicted with an cervical cancer. In this method, a protein or peptide comprising the entirety or a segment of a marker protein is synthesized or isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein or peptide *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the protein or peptide. The vertebrate may optionally (and preferably) be immunized at least one additional time with the protein or peptide, so that the vertebrate exhibits a robust immune response to the protein or peptide. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the marker protein or a fragment thereof. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test compound for inhibiting cervical cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of cervical cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of cervical cells, it is likewise recognized that changes in the levels of expression of other of the markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit an cervical cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous cervical cells).

This method thus comprises comparing expression of a marker in a first cervical cell sample and maintained in the presence of the test compound and expression of the marker in a second cervical cell sample and maintained in the absence of the test compound. A significantly reduced expression of a marker of the invention in the presence of the test compound is an indication that the test compound inhibits cervical cancer. The cervical cell samples may, for example, be aliquots of a single sample of normal cervical cells obtained from a patient, pooled samples of normal cervical cells obtained from a patient, cells of a normal cervical cell line, aliquots of a single sample of cervical cancer cells obtained from a patient, pooled samples of cervical cancer cells obtained from a patient, cells of an cervical cancer cell line, or the like. In one embodiment, the samples are cervical cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various cervical cancers are tested in order to identify the compound which is likely to best inhibit the cervical cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting cervical cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significantly lower level of expression of a marker of the invention then the therapy is efficacious for inhibiting cervical cancer. As above, if samples from a selected patient are used in this method,

then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be efficacious for inhibiting cervical cancer in the patient.

As described above, the cancerous state of human cervical cells is correlated with changes in the levels of expression of the markers of the invention. The invention includes a method for assessing the human cervical cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human cervical cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significantly higher level of expression of a marker of the invention in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human cervical cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules, including nucleic acids which encode a marker protein or a portion thereof. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify marker nucleic acid molecules, and fragments of marker nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or mutation of marker nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*,

sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

10 A nucleic acid molecule of the present invention can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 15 1989).

 A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can 20 be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, nucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

 In another preferred embodiment, an isolated nucleic acid molecule of the 25 invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a marker nucleic acid or to the nucleotide sequence of a nucleic acid encoding a marker protein. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given 30 nucleotide sequence thereby forming a stable duplex.

 Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker nucleic acid or which encodes a marker protein. Such nucleic acids

can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150,
5 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, *e.g.*, a
10 radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

15 The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), and thus encode the same protein.

It will be appreciated by those skilled in the art that DNA sequence
20 polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist
25 that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic
30 acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be

readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

5 In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a marker nucleic acid or to a nucleic acid encoding a marker protein. As
10 used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons,
15 N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

In addition to naturally-occurring allelic variants of a nucleic acid molecule of the invention that can exist in the population, the skilled artisan will further
20 appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from
25 the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration. Alternatively, amino acid residues that are conserved among the homologs of various
30 species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a variant marker protein that contain changes in amino acid residues that are not essential for activity. Such variant marker proteins differ in amino acid sequence from the naturally-occurring marker proteins, yet retain biological activity. In one embodiment, such a variant marker protein has an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of a marker protein.

An isolated nucleic acid molecule encoding a variant marker protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of marker nucleic acids, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded marker cDNA molecule or complementary to a marker mRNA sequence. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand,

or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a marker protein. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences
5 which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an
10 antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which
15 can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-
20 methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-
25 methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense
30 orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a marker protein to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into an ovary-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α -units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-O-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a marker protein can be designed based

upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742).

- 5 Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a marker of the invention can be inhibited
10 by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the marker nucleic acid or protein (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

- 15 In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used
20 herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be
25 performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific
30 modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup

(1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the
5 formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and
10 specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support
15 using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*,
20 1996, *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975, *Bioorganic Med. Chem. Lett.* 5:1119-1124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents
25 facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques*
30 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated marker proteins and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a marker protein or a fragment thereof. In one embodiment, the native marker protein can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, a protein or peptide comprising the whole or a segment of the marker protein is produced by recombinant DNA techniques. Alternative to recombinant expression, such protein or peptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less

than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such
5 preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a marker protein include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the marker protein, which include fewer amino acids than the full
10 length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding full-length protein. A biologically active portion of a marker protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in
15 which other regions of the marker protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of the marker protein.

Preferred marker proteins are encoded by nucleotide sequences comprising the sequence of any of the sequences set forth in the Sequence Listing.
20 Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the corresponding naturally-occurring marker protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two
25 nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid
30 residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, %

identity = # of identical positions/total # of positions (*e.g.*, overlapping positions) x100).
In one embodiment the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a
5 mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with
10 the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called
15 Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the
20 respective programs (*e.g.*, BLASTX and BLASTN) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software
25 package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for
30 comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins comprising a marker protein or a segment thereof. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a marker protein operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the marker protein). Within the fusion protein, the term "operably linked" is intended to indicate that the marker protein or segment thereof and the heterologous polypeptide are fused in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the marker protein or segment.

One useful fusion protein is a GST fusion protein in which a marker protein or segment is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a marker protein can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook *et al.*, *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a marker protein is fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a marker protein. Inhibition of ligand/receptor interaction can be

useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a marker protein in a subject, to purify ligands and in screening assays
5 to identify molecules which inhibit the interaction of the marker protein with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, *e.g.*, Ausubel *et al.*, *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an
15 expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of marker proteins. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one
20 or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to marker proteins, fusion proteins or segments thereof having a signal sequence, as well as to such proteins from which the signal sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one
25 embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a marker protein or a segment thereof. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the
30 extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the marker proteins.

Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function.

5 Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

Variants of a marker protein which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the marker proteins from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, 1983, *Tetrahedron* 39:3; Itakura *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

15 20 25

In addition, libraries of segments of a marker protein can be used to generate a variegated population of polypeptides for screening and subsequent selection of variant marker proteins or segments thereof. For example, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different

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nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

5 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,
10 transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify
15 variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

 Another aspect of the invention pertains to antibodies directed against a protein of the invention. In preferred embodiments, the antibodies specifically bind a marker protein or a fragment thereof. The terms "antibody" and "antibodies" as used
20 interchangeably herein refer to immunoglobulin molecules as well as fragments and derivatives thereof that comprise an immunologically active portion of an immunoglobulin molecule, (*i.e.*, such a portion contains an antigen binding site which specifically binds an antigen, such as a marker protein, *e.g.*, an epitope of a marker protein). An antibody which specifically binds to a protein of the invention is an
25 antibody which binds the protein, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the protein. Examples of an immunologically active portion of an immunoglobulin molecule include, but are not limited to, single-chain antibodies (scAb), F(ab) and F(ab')₂ fragments.

 An isolated protein of the invention or a fragment thereof can be used as
30 an immunogen to generate antibodies. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the

proteins of the invention, and encompasses at least one epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions. In preferred embodiments, an isolated marker protein or fragment thereof is used as an immunogen.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized protein or peptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent. Preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a protein of the invention. In such a manner, the resulting antibody compositions have reduced or no binding of human proteins other than a protein of the invention.

The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope. Preferred polyclonal and monoclonal antibody compositions are ones that have been selected for antibodies directed against a protein of the invention. Particularly preferred polyclonal and monoclonal antibody preparations are ones that contain only antibodies directed against a marker protein or fragment thereof.

Polyclonal antibodies can be prepared by immunizing a suitable subject with a protein of the invention as an immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. At an appropriate time after immunization, *e.g.*, when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies (mAb) by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell

hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology*, Coligan *et al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a protein of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275-1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

The invention also provides recombinant antibodies that specifically bind a protein of the invention. In preferred embodiments, the recombinant antibodies specifically binds a marker protein or fragment thereof. Recombinant antibodies include, but are not limited to, chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, single-chain antibodies and multi-specific antibodies. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly *et al.*, U.S. Patent No. 4,816,567; and Boss *et al.*, U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Single-chain antibodies have an

antigen binding site and consist of a single polypeptide. They can be produced by techniques known in the art, for example using methods described in Ladner *et al.* U.S. Pat. No. 4,946,778 (which is incorporated herein by reference in its entirety); Bird *et al.*, (1988) *Science* 242:423-426; Whitlow *et al.*, (1991) *Methods in Enzymology* 2:1-9; 5 Whitlow *et al.*, (1991) *Methods in Enzymology* 2:97-105; and Huston *et al.*, (1991) *Methods in Enzymology Molecular Design and Modeling: Concepts and Applications* 203:46-88. Multi-specific antibodies are antibody molecules having at least two antigen-binding sites that specifically bind different antigens. Such molecules can be produced by techniques known in the art, for example using methods described in Segal, 10 U.S. Patent No. 4,676,980 (the disclosure of which is incorporated herein by reference in its entirety); Holliger *et al.*, (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Whitlow *et al.*, (1994) *Protein Eng.* 7:1017-1026 and U.S. Pat. No. 6,121,424.

Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human 15 species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 20 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521-3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) 25 *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

More particularly, humanized antibodies can be produced, for example, 30 using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal

antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

The antibodies of the invention can be isolated after production (e.g., from the blood or serum of the subject) or synthesis and further purified by well-known techniques. For example, IgG antibodies can be purified using protein A chromatography. Antibodies specific for a protein of the invention can be selected or (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is

contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein of the invention.

In a preferred embodiment, the substantially purified antibodies of the invention may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a protein of the invention. In a particularly preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a protein of the invention. In a more preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a marker protein.

An antibody directed against a protein of the invention can be used to isolate the protein by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker protein or fragment thereof (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in a cervical-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by the use of an antibody derivative, which comprises an antibody of the invention coupled to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Antibodies of the invention may also be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having an cervical cancer. In another preferred embodiment, antibodies that bind

5 specifically to a marker protein or fragment thereof are used for therapeutic treatment. Further, such therapeutic antibody may be an antibody derivative or immunotoxin comprising an antibody conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D,

10 ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate,

15 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*,

20 dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugated antibodies of the invention can be used for modifying a given biological response, for the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or

25 polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as ribosome-inhibiting protein (see Better et al., U.S. Patent No. 6,146,631, the disclosure of which is incorporated herein in its entirety), abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor,

30 tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophase colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug
5 Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in
10 *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982).

Accordingly, in one aspect, the invention provides substantially purified antibodies, antibody fragments and derivatives, all of which specifically bind to a
15 protein of the invention and preferably, a marker protein. In various embodiments, the substantially purified antibodies of the invention, or fragments or derivatives thereof, can be human, non-human, chimeric and/or humanized antibodies. In another aspect, the invention provides non-human antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein.
20 Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies. In still a further aspect, the invention provides monoclonal antibodies, antibody fragments and derivatives, all of
25 which specifically bind to a protein of the invention and preferably, a marker protein. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the
30 invention is a pharmaceutical composition comprising an antibody of the invention. In one embodiment, the pharmaceutical composition comprises an antibody of the invention and a pharmaceutically acceptable carrier.

III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a marker protein (or a portion of such a protein). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and

those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

The recombinant expression vectors of the invention can be designed for expression of a marker protein or a segment thereof in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA

polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage
5 harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another
10 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

15 In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

20 Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in
25 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.*, 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2,
30 cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al.*, *supra*.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable
5 tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters
10 (e.g., the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters
15 (Kessel and Gruss, 1990, *Science* 249:374-379) and the α -fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory
20 sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or
25 enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the
30 vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential
5 progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*,
10 insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium
15 phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells
20 may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid
25 can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a marker protein or a segment thereof. Accordingly, the invention further provides methods for producing a marker protein or a segment
30 thereof using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding a marker protein or a segment thereof has been introduced) in a suitable medium such that the is produced. In another embodiment, the method further

comprises isolating the marker protein or a segment thereof from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a
5 fertilized oocyte or an embryonic stem cell into which a sequences encoding a marker protein or a segment thereof have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a marker protein have been
10 altered. Such animals are useful for studying the function and/or activity of the marker protein and for identifying and/or evaluating modulators of marker protein. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human
15 primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-
20 human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a
25 nucleic acid encoding a marker protein into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the
30 transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Patent No.

4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA
5 encoding the transgene in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which
10 contains at least a portion of a gene encoding a marker protein into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector
15 can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for
20 homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a
25 description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (see, *e.g.*, Bradley,
30 *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed

animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication
5 NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso *et al.* (1992) *Proc.*
10 *Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a
selected protein are required. Such animals can be provided through the construction of
15 "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-
20 813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical
25 compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical
30 administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is

contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a marker nucleic acid or protein. Such methods comprise formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a marker nucleic acid or protein. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or activity of a marker nucleic acid or protein and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.* 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while

the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al.*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al.*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a protein encoded by or corresponding to a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a protein encoded by or corresponding to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a protein can be accomplished, for example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (*e.g.*, marker substrates) can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the expression of a marker or the activity of a protein encoded by or corresponding to a marker, or a biologically active portion

thereof. In all likelihood, the protein encoded by or corresponding to the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker
5 "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of a protein encoded by or corresponding to marker to identify the protein's natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein
10 as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent No. 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al*, 1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly
15 involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker protein or downstream elements of a marker protein-mediated signaling pathway. Alternatively, such marker protein binding partners may also be found to be inhibitors of the marker protein.

The two-hybrid system is based on the modular nature of most
20 transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is
25 fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to
30 the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.*, affect either positively or negatively) interactions between a marker protein and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an cervical cancer marker protein identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker protein and its binding partner involves preparing a reaction mixture containing the marker protein and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker protein and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the marker protein and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker protein and its binding partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance interaction of the marker protein and its binding partner.

The assay for compounds that interfere with the interaction of the marker protein with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker protein or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds

that interfere with the interaction between the marker proteins and the binding partners (e.g., by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test compounds that disrupt preformed complexes, *e.g.*, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker protein or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker protein or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (*e.g.*, physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker protein or a marker protein binding partner can be immobilized utilizing conjugation of biotin and

streptavidin. Biotinylated marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the
5 protein-immobilized surfaces can be prepared in advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (*e.g.*, by washing) and any complexes formed will remain immobilized on the solid
10 surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for
15 the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may
20 be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test
25 compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and
30 immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993

Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, *e.g.*, Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York, 1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, nondenaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel *et al* (eds.), In: Current Protocols in Molecular Biology, J. Wiley & Sons, New York, 1999). In this technique, all proteins binding to an antibody specific to one of the binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be compared, thus offering information about the ability of the compound to modulate interactions between the marker protein and its binding partner.

Also within the scope of the present invention are methods for direct detection of interactions between the marker protein and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer
5 may be utilized (see, *e.g.*, Lakowicz *et al*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al*, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.*, marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.*, marker or test compound), which in turn is able to fluoresce
10 due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships
15 between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in
20 the preformed complex will result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression
25 of marker mRNA or protein in the cell, is determined. The level of expression of marker mRNA or protein in the presence of the candidate compound is compared to the level of expression of marker mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA
30 or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA or protein is less (statistically significantly less) in the presence of the candidate compound

than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA or protein.

5 In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

10 This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a marker modulating agent, an antisense marker nucleic acid molecule, a marker-specific antibody, or a marker-binding
15 partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

20 It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to
25 be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1
30 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or

about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents
5 is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend
10 upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be
15 compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline
20 solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with
25 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the
30 extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy

syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

15 Sterile injectable solutions can be prepared by incorporating the active compound (e.g., a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium, and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

25 Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed.

30 Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a

binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as
5 peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal
10 means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal
15 administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

20 In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid.
25 Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled
30 in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the

subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the cervical epithelium). A method for lipidation of antibodies is described by Cruikshank *et al.* (1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193.

The invention also provides vaccine compositions for the prevention and/or treatment of cervical cancer. The invention provides cervical cancer vaccine compositions in which a protein of a marker of Table 1, or a combination of proteins of the markers of Table 1, are introduced into a subject in order to stimulate an immune response against the cervical cancer. The invention also provides cervical cancer vaccine compositions in which a gene expression construct, which expresses a marker or fragment of a marker identified in Table 1, is introduced into the subject such that a protein or fragment of a protein encoded by a marker of Table 1 is produced by transfected cells in the subject at a higher than normal level and elicits an immune response.

In one embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the prevention of cervical cancer. In another embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the treatment of cervical cancer.

By way of example, a cervical cancer vaccine comprised of the proteins of the markers of Table 1, may be employed for the prevention and/or treatment of cervical cancer in a subject by administering the vaccine by a variety of routes, *e.g.*, intradermally, subcutaneously, or intramuscularly. In addition, the cervical cancer

vaccine can be administered together with adjuvants and/or immunomodulators to boost the activity of the vaccine and the subject's response. In one embodiment, devices and/or compositions containing the vaccine, suitable for sustained or intermittent release could be, implanted in the body or topically applied thereto for the relatively slow
5 release of such materials into the body. The cervical cancer vaccine can be introduced along with immunomodulatory compounds, which can alter the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

In another embodiment, a cervical cancer vaccine comprised of an
10 expression construct of the markers of Table 1, may be introduced by injection into muscle or by coating onto microprojectiles and using a device designed for the purpose to fire the projectiles at high speed into the skin. The cells of the subject will then express the protein(s) or fragments of proteins of the markers of Table 1 and induce an immune
15 response. In addition, the cervical cancer vaccine may be introduced along with expression constructs for immunomodulatory molecules, such as cytokines, which may increase the immune response or modulate the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

The marker nucleic acid molecules can be inserted into vectors and used
20 as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, *e.g.*, Chen *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which
25 the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or
30 dispenser together with instructions for administration.

V. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic
5 assays for determining the level of expression of one or more marker proteins or nucleic acids, in order to determine whether an individual is at risk of developing cervical cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit cervical cancer or to treat or prevent any other disorder {*i.e.* in order to understand any cervical carcinogenic effects that such treatment may have}) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further
15 detail in the following sections.

A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a marker protein or nucleic acid in a biological sample involves obtaining a biological sample
20 (*e.g.* a cervical-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for
25 detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a marker protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a marker protein include introducing
30 into a subject a labeled antibody directed against the protein or fragment thereof. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

5 It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon
10 excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label
15 may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured
20 through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

 In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis
25 (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345 and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index
30 of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to:

5 differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7).

10 Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively

15 different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, *e.g.*, Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 20 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this

25 technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of marker mRNA can be

30 determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA.

For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from cervical cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be
5 processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain
10 reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and
15 sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted
20 with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level
25 of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA marker in a sample involves the process of nucleic acid amplification, *e.g.*, by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained
30 sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid

amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being
5 a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid
10 molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the cervical cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that
15 encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a
20 gene that is not a marker, *e.g.*, a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, *e.g.*, a patient sample, to another sample, *e.g.*, a non-cervical cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed
25 in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.
30

Preferably, the samples used in the baseline determination will be from cervical cancer or from non-cervical cancer cells of cervical tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker
5 assayed is cervical specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cervical cells provides a means for grading the severity of the cervical cancer state.

In another embodiment of the present invention, a marker protein is
10 detected. A preferred agent for detecting marker protein of the invention is an antibody capable of binding to such a protein or a fragment thereof, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment or derivative thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct
15 labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with
20 fluorescently labeled streptavidin.

Proteins from cervical cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring
25 Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can
30 readily adapt known protein/antibody detection methods for use in determining whether cervical cells express a marker of the present invention.

In one format, antibodies, or antibody fragments or derivatives, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody or proteins on a solid support. Suitable solid phase supports or carriers include
5 any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present
10 invention. For example, protein isolated from cervical cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of
15 bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a marker protein or nucleic acid in a biological sample (*e.g.*, cervical smear). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing cervical cancer. For example, the kit can comprise a labeled compound or
20 agent capable of detecting a marker protein or nucleic acid in a biological sample and means for determining the amount of the protein or mRNA in the sample (*e.g.*, an antibody which binds the protein or a fragment thereof, or an oligonucleotide probe which binds to DNA or mRNA encoding the protein). Kits can also include instructions for interpreting the results obtained using the kit.

25 For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a marker protein; and, optionally, (2) a second, different antibody which binds to either the protein or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an
30 oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a marker protein or (2) a pair of primers useful for amplifying a marker nucleic acid molecule. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components

necessary for detecting the detectable label (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package,
5 along with instructions for interpreting the results of the assays performed using the kit.

B. Pharmacogenomics

The markers of the invention are also useful as pharmacogenomic markers. As used herein, a "pharmacogenomic marker" is an objective biochemical
10 marker whose expression level correlates with a specific clinical drug response or susceptibility in a patient (see, e.g., McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker expression is related to the predicted response of the patient and more particularly the patient's tumor to therapy with a specific drug or class of drugs. By assessing the presence or quantity of
15 the expression of one or more pharmacogenomic markers in a patient, a drug therapy which is most appropriate for the patient, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein encoded by specific tumor markers in a patient, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be
20 present in the patient. The use of pharmacogenomic markers therefore permits selecting or designing the most appropriate treatment for each cancer patient without trying different drugs or regimes.

Another aspect of pharmacogenomics deals with genetic conditions that alters the way the body acts on drugs. These pharmacogenetic conditions can occur
25 either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes
30 is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show

exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for cervical cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the

level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased expression of the marker gene(s) during the course of treatment may indicate ineffective dosage and the desirability of increasing the dosage. Conversely, decreased expression of the marker gene(s) may indicate efficacious treatment and no need to change dosage.

10 D. Electronic Apparatus Readable Media and Arrays

Electronic apparatus readable media comprising a marker of the present invention is also provided. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be read and accessed directly by an electronic apparatus. Such media can include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as compact disc; electronic storage media such as RAM, ROM, EPROM, EEPROM and the like; general hard disks and hybrids of these categories such as magnetic/optical storage media. The medium is adapted or configured for having recorded thereon a marker of the present invention.

20 As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; networks, including a local area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet; electronic appliances such as a personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems.

As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known media to generate manufactures comprising the markers of the present invention.

30 A variety of software programs and formats can be used to store the marker information of the present invention on the electronic apparatus readable medium. For example, the marker nucleic acid sequence can be represented in a word

processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like, as well as in other forms. Any number of data processor structuring formats (*e.g.*, text file or database) may be
5 employed in order to obtain or create a medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the
10 present invention in readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The present invention therefore provides a medium for holding
15 instructions for performing a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, wherein the method comprises the steps of determining the presence or absence of a marker and based on the presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer and/or recommending a particular treatment for cervical cancer or pre-
20 cervical cancer condition.

The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker wherein the method comprises the steps of determining the presence or absence of the marker, and based on the
25 presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer, and/or recommending a particular treatment for the cervical cancer or pre-cervical cancer condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

30 The present invention also provides in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker, said method comprising the steps of receiving information associated with the marker receiving phenotypic information associated with the subject,

acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has a cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of
5 recommending a particular treatment for the cervical cancer or pre-cervical cancer condition.

The present invention also provides a business method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, said method comprising the steps of receiving information associated with the marker, receiving
10 phenotypic information associated with the subject, acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of recommending a particular treatment for the
15 cervical cancer or pre-cervical cancer condition.

The invention also includes an array comprising a marker of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes
20 can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be
25 grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a
30 determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the

opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

5 In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of cervical cancer, progression of cervical cancer, and processes, such a cellular transformation associated with cervical cancer.

10 The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

 The array is also useful for ascertaining differential expression patterns of
15 one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

E. Surrogate Markers

 The markers of the invention may serve as surrogate markers for one or
20 more disorders or disease states or for conditions leading up to disease states, and in particular, cervical cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the
25 disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is
30 reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate

markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a “pharmacodynamic marker” is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

VI. Experimental Protocol

A. Identification of clones

Cervical tumor specific cDNA clones were identified by transcription profiling using mRNA from 12 cervical tumors, 5 CIN III, 5 CIN I and 12 normal
5 cervical tissues. The subtracted libraries were constructed using mRNA from at least three independent normal ectocervix, B-lymphocytes, T-lymphocytes and other white blood cells (in activated and resting states) as drivers and four independent stage 1B cervical tumors or four independent CIN III cervical samples as testers. The top up-regulated clones in tumors or CIN III cervical tissues, as determined by proprietary
10 statistical analysis methods, were selected. The clusters in which the selected clones belong were blasted against both public and proprietary sequence databases in order to identify other EST sequences or clusters with significant overlap. Thus, contiguous EST sequences and/or clusters were assembled into full-length genes.

An identification of protein sequence corresponding to the clone was
15 accomplished by obtaining one of the following:

- a) a direct match between the protein sequence and at least one EST sequence in one of its 6 possible translations;
- b) a direct match between the nucleotide sequence for the mRNA corresponding to the protein sequence and at least one EST sequence;
- 20 c) a match between the protein sequence and a contiguous assembly (contig) of the EST sequences with other available EST sequences in the databases in one of its 6 possible translations; or
- d) a match between the nucleotide sequence for the mRNA corresponding to the protein sequence and a contiguous assembly of the EST sequences with other
25 available EST sequences in the databases in one of its 6 possible translations.

VII. Summary of the Data

Tables 1-3 list the markers obtained using the foregoing protocol. The tables provide the name of the gene corresponding to the marker ("Gene Name"), the
30 sequence listing identifier of the cDNA sequence of a nucleotide transcript encoded by or corresponding to the marker ("SEQ ID NO (nts)"), the sequence listing identifier of the amino acid sequence of a protein encoded by the nucleotide transcript ("SEQ ID NO

(AAs”)), and the location of the protein coding sequence within the cDNA sequence (“CDS”).

Table 1 lists all of the markers of the invention which are over-expressed in cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells. Table 2
5 lists newly-identified nucleotide and amino acid sequences useful as cervical cancer markers. Table 3 lists newly-identified nucleotide sequences useful as cervical cancer markers.

Other Embodiments

10 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims:

What is claimed:

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151,
5 167, 203, 217, 231, 233, 51, 65, 67, 68, 100, and 153.
2. A vector which contains the nucleic acid molecule of claim 1.
3. A host cell which contains the nucleic acid molecule of claim 1.
- 10 4. A method of assessing whether a patient is afflicted with cervical cancer, the method comprising comparing:
 - a) the level of expression of a marker in a patient sample, wherein the marker is selected from Table 1; and
 - 15 b) the normal level of expression of the marker in a control non-cervical cancer sample,wherein a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer.
- 20 5. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151, 167, 203, 217, 231, and 233.
- 25 6. An antibody which selectively binds to the polypeptide of claim 5.
7. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 144, 146, 148, 150, 152, 168, 204, 218, 232, and 234.
- 30 8. An antibody which selectively binds to the polypeptide of claim 7.

SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc. et al.

<120> NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
OF CERVICAL CANCER

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<151> 2001-06-13

<150> US 60/298,155

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Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu						
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Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu						
	1570		1575		1580	
Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu						
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Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg						
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Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu						
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Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys						
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Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu Glu Gly Asn Glu Lys Lys		2640
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Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro Gln Asp Val Glu Val Leu		
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Lys Thr Thr Thr Glu Leu Phe His Ser Asn Glu Glu Ser Gly Phe Phe		
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Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser Val Ala Thr Lys Ala Glu		
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Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
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Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu
625					630					635					640
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys
				645					650					655	
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn
			660					665					670		
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu
			675				680					685			
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp
			690				695				700				
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln
705					710					715					720
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys
				725					730					735	
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr
			740					745					750		
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu
		755					760					765			
Lys	Phe	Ala	Gln	Leu	Glu	Ala	Glu	Asn	Ser	Ile	Leu	Lys	Asp	Glu	Lys
		770				775					780				
Lys	Thr	Leu	Glu	Asp	Met	Leu	Lys	Ile	His	Thr	Pro	Val	Ser	Gln	Glu
785					790					795					800
Glu	Arg	Leu	Ile	Phe	Leu	Asp	Ser	Ile	Lys	Ser	Lys	Ser	Lys	Asp	Ser
				805					810					815	
Val	Trp	Glu	Lys	Glu	Ile	Glu	Ile	Leu	Ile	Glu	Glu	Asn	Glu	Asp	Leu
			820					825					830		
Lys	Gln	Gln	Cys	Ile	Gln	Leu	Asn	Glu	Glu	Ile	Glu	Lys	Gln	Arg	Asn

835	840	845
Thr Phe Ser Phe Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu		
850	855	860
Gln Glu Glu Tyr Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp		
865	870	875
Ser Lys Asn Lys Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu		
885	890	895
Asn Glu Glu Leu His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met		
900	905	910
Lys Ser Ser Val Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu		
915	920	925
Glu Met Gly Glu Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys		
930	935	940
Leu Glu Val Thr Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser		
945	950	955
Asp Leu Ser Glu Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu		
965	970	975
Asn Glu Glu Val Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu		
980	985	990
Arg Cys Arg Glu Leu Glu Ile Ile Ile Asn His Asn Arg Ala Glu Asn		
995	1000	1005
Val Gln Ser Cys Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val Val		
1010	1015	1020
Thr Met Thr Ser Arg Gly Ala Glu Gly Ser Val Ser Lys Val Asn Lys		
1025	1030	1035
Ser Phe Gly Glu Glu Ser Lys Ile Met Val Glu Asp Lys Val Ser Phe		
1045	1050	1055
Glu Asn Met Thr Val Gly Glu Glu Ser Lys Gln Glu Gln Leu Ile Leu		
1060	1065	1070
Asp His Leu Pro Ser Val Thr Lys Glu Ser Ser Leu Arg Ala Thr Gln		
1075	1080	1085
Pro Ser Glu Asn Asp Lys Leu Gln Lys Glu Leu Asn Val Leu Lys Ser		
1090	1095	1100
Glu Gln Asn Asp Leu Arg Leu Gln Met Glu Ala Gln Arg Ile Cys Leu		
1105	1110	1115
Ser Leu Val Tyr Ser Thr His Val Asp Gln Val Arg Glu Tyr Met Glu		
1125	1130	1135
Asn Glu Lys Asp Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu Ile Phe		
1140	1145	1150
Ala Gln Glu Glu Lys Ile Lys Glu Leu Gln Lys Ile His Gln Leu Glu		
1155	1160	1165
Leu Gln Thr Met Lys Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu		
1170	1175	1180
His Leu Leu Ile Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser		
1185	1190	1195
Tyr Phe Leu Gln Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro		
1205	1210	1215
Ala Leu Lys Cys Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp		
1220	1225	1230
Tyr Ile Ser Glu Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg Tyr Glu		
1235	1240	1245
Val Gln Asp Phe Gln Glu Asn Met His Thr Leu Leu Asn Lys Val Thr		
1250	1255	1260
Glu Glu Tyr Asn Lys Leu Leu Val Leu Gln Thr Arg Leu Ser Lys Ile		
1265	1270	1275
Trp Gly Gln Gln Thr Asp Gly Met Lys Leu Glu Phe Gly Glu Glu Asn		
1285	1290	1295
Leu Pro Lys Glu Glu Thr Glu Phe Leu Ser Ile His Ser Gln Met Thr		
1300	1305	1310

Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu
 1315 1320 1325
 Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu
 1330 1335 1340
 Ser Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn
 1345 1350 1355 1360
 Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser
 1365 1370 1375
 Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr
 1380 1385 1390
 Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys
 1395 1400 1405
 Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu
 1410 1415 1420
 Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu
 1425 1430 1435 1440
 Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala
 1445 1450 1455
 Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala
 1460 1465 1470
 Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe
 1475 1480 1485
 Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu
 1490 1495 1500
 Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu
 1505 1510 1515 1520
 Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His
 1525 1530 1535
 Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met
 1540 1545 1550
 Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu
 1555 1560 1565
 Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu
 1570 1575 1580
 Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu
 1585 1590 1595 1600
 His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met
 1605 1610 1615
 Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg
 1620 1625 1630
 Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu
 1635 1640 1645
 Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys
 1650 1655 1660
 Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn
 1665 1670 1675 1680
 Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu
 1685 1690 1695
 Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val
 1700 1705 1710
 Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn
 1715 1720 1725
 Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala
 1730 1735 1740
 Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser
 1745 1750 1755 1760
 Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu
 1765 1770 1775
 Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp

1780					1785					1790						
Glu	Ser	Ile	Pro	Ser	Tyr	Ser	Gly	Ser	Asp	Met	Pro	Arg	Asn	Asp	Ile	
1795					1800					1805						
Asn	Met	Trp	Ser	Lys	Val	Thr	Glu	Glu	Gly	Thr	Glu	Leu	Ser	Gln	Arg	
1810					1815					1820						
Leu	Val	Arg	Ser	Gly	Phe	Ala	Gly	Thr	Glu	Ile	Asp	Pro	Glu	Asn	Glu	
1825					1830					1835					1840	
Glu	Leu	Met	Leu	Asn	Ile	Ser	Ser	Arg	Leu	Gln	Ala	Ala	Val	Glu	Lys	
1845					1850					1855						
Leu	Leu	Glu	Ala	Ile	Ser	Glu	Thr	Ser	Ser	Gln	Leu	Glu	His	Ala	Lys	
1860					1865					1870						
Val	Thr	Gln	Thr	Glu	Leu	Met	Arg	Glu	Ser	Phe	Arg	Gln	Lys	Gln	Glu	
1875					1880					1885						
Ala	Thr	Glu	Ser	Leu	Lys	Cys	Gln	Glu	Glu	Leu	Arg	Glu	Arg	Leu	His	
1890					1895					1900						
Glu	Glu	Ser	Arg	Ala	Arg	Glu	Gln	Leu	Ala	Val	Glu	Leu	Ser	Lys	Ala	
1905					1910					1915					1920	
Glu	Gly	Val	Ile	Asp	Gly	Tyr	Ala	Asp	Glu	Lys	Thr	Leu	Phe	Glu	Arg	
1925					1930					1935						
Gln	Ile	Gln	Glu	Lys	Thr	Asp	Ile	Ile	Asp	Arg	Leu	Glu	Gln	Glu	Leu	
1940					1945					1950						
Leu	Cys	Ala	Ser	Asn	Arg	Leu	Gln	Glu	Leu	Glu	Ala	Glu	Gln	Gln	Gln	
1955					1960					1965						
Ile	Gln	Glu	Glu	Arg	Glu	Leu	Ser	Arg	Gln	Lys	Glu	Ala	Met	Lys		
1970					1975					1980						
Ala	Glu	Ala	Gly	Pro	Val	Glu	Gln	Gln	Leu	Leu	Gln	Glu	Thr	Glu	Lys	
1985					1990					1995					2000	
Leu	Met	Lys	Glu	Lys	Leu	Glu	Val	Gln	Cys	Gln	Ala	Glu	Lys	Val	Arg	
2005					2010					2015						
Asp	Asp	Leu	Gln	Lys	Gln	Val	Lys	Ala	Leu	Glu	Ile	Asp	Val	Glu	Glu	
2020					2025					2030						
Gln	Val	Ser	Arg	Phe	Ile	Glu	Leu	Glu	Gln	Glu	Lys	Asn	Thr	Glu	Leu	
2035					2040					2045						
Met	Asp	Leu	Arg	Gln	Gln	Asn	Gln	Ala	Leu	Glu	Lys	Gln	Leu	Glu	Lys	
2050					2055					2060						
Met	Arg	Lys	Phe	Leu	Asp	Glu	Gln	Ala	Ile	Asp	Arg	Glu	His	Glu	Arg	
2065					2070					2075					2080	
Asp	Val	Phe	Gln	Gln	Glu	Ile	Gln	Lys	Leu	Glu	Gln	Gln	Leu	Lys	Val	
2085					2090					2095						
Val	Pro	Arg	Phe	Gln	Pro	Ile	Ser	Glu	His	Gln	Thr	Arg	Glu	Val	Glu	
2100					2105					2110						
Gln	Leu	Ala	Asn	His	Leu	Lys	Glu	Lys	Thr	Asp	Lys	Cys	Ser	Glu	Leu	
2115					2120					2125						
Leu	Leu	Ser	Lys	Glu	Gln	Leu	Gln	Arg	Asp	Ile	Gln	Glu	Arg	Asn	Glu	
2130					2135					2140						
Glu	Ile	Glu	Lys	Leu	Glu	Phe	Arg	Val	Arg	Glu	Leu	Glu	Gln	Ala	Leu	
2145					2150					2155					2160	
Leu	Val	Glu	Asp	Arg	Lys	His	Phe	Gly	Ala	Val	Glu	Ala	Lys	Pro	Glu	
2165					2170					2175						
Leu	Ser	Leu	Glu	Val	Gln	Leu	Gln	Ala	Glu	Arg	Asp	Ala	Ile	Asp	Arg	
2180					2185					2190						
Lys	Glu	Lys	Glu	Ile	Thr	Asn	Leu	Glu	Glu	Gln	Leu	Glu	Gln	Phe	Arg	
2195					2200					2205						
Glu	Glu	Leu	Glu	Asn	Lys	Asn	Glu	Glu	Val	Gln	Gln	Leu	His	Met	Gln	
2210					2215					2220						
Leu	Glu	Ile	Gln	Lys	Lys	Glu	Ser	Thr	Thr	Arg	Leu	Gln	Glu	Leu	Glu	
2225					2230					2235					2240	
Gln	Glu	Asn	Lys	Leu	Phe	Lys	Asp	Asp	Met	Glu	Lys	Leu	Gly	Leu	Ala	
2245					2250					2255						

Ile	Lys	Glu	Ser	Asp	Ala	Met	Ser	Thr	Gln	Asp	Gln	His	Val	Leu	Phe	2260	2265	2270
Gly	Lys	Phe	Ala	Gln	Ile	Ile	Gln	Glu	Lys	Glu	Val	Glu	Ile	Asp	Gln	2275	2280	2285
Leu	Asn	Glu	Gln	Val	Thr	Lys	Leu	Gln	Gln	Gln	Leu	Lys	Ile	Thr	Thr	2290	2295	2300
Asp	Asn	Lys	Val	Ile	Glu	Glu	Lys	Asn	Glu	Leu	Ile	Arg	Asp	Leu	Glu	2305	2310	2315
Thr	Gln	Ile	Glu	Cys	Leu	Met	Ser	Asp	Gln	Glu	Cys	Val	Lys	Arg	Asn	2325	2330	2335
Arg	Glu	Glu	Glu	Ile	Glu	Gln	Leu	Asn	Glu	Val	Ile	Glu	Lys	Leu	Gln	2340	2345	2350
Gln	Glu	Leu	Ala	Asn	Ile	Gly	Gln	Lys	Thr	Ser	Met	Asn	Ala	His	Ser	2355	2360	2365
Leu	Ser	Glu	Glu	Ala	Asp	Ser	Leu	Lys	His	Gln	Leu	Asp	Val	Val	Ile	2370	2375	2380
Ala	Glu	Lys	Leu	Ala	Leu	Glu	Gln	Gln	Val	Glu	Thr	Ala	Asn	Glu	Glu	2385	2390	2395
Met	Thr	Phe	Met	Lys	Asn	Val	Leu	Lys	Glu	Thr	Asn	Phe	Lys	Met	Asn	2405	2410	2415
Gln	Leu	Thr	Gln	Glu	Leu	Phe	Ser	Leu	Lys	Arg	Glu	Arg	Glu	Ser	Val	2420	2425	2430
Glu	Lys	Ile	Gln	Ser	Ile	Pro	Glu	Asn	Ser	Val	Asn	Val	Ala	Ile	Asp	2435	2440	2445
His	Leu	Ser	Lys	Asp	Lys	Pro	Glu	Leu	Glu	Val	Val	Leu	Thr	Glu	Asp	2450	2455	2460
Ala	Leu	Lys	Ser	Leu	Glu	Asn	Gln	Thr	Tyr	Phe	Lys	Ser	Phe	Glu	Glu	2465	2470	2475
Asn	Gly	Lys	Gly	Ser	Ile	Ile	Asn	Leu	Glu	Thr	Arg	Leu	Leu	Gln	Leu	2485	2490	2495
Glu	Ser	Thr	Val	Ser	Ala	Lys	Asp	Leu	Glu	Leu	Thr	Gln	Cys	Tyr	Lys	2500	2505	2510
Gln	Ile	Lys	Asp	Met	Gln	Glu	Gln	Gly	Gln	Phe	Glu	Thr	Glu	Met	Leu	2515	2520	2525
Gln	Lys	Lys	Ile	Val	Asn	Leu	Gln	Lys	Ile	Val	Glu	Glu	Lys	Val	Ala	2530	2535	2540
Ala	Ala	Leu	Val	Ser	Gln	Ile	Gln	Leu	Glu	Ala	Val	Gln	Glu	Tyr	Ala	2545	2550	2555
Lys	Phe	Cys	Gln	Asp	Asn	Gln	Thr	Ile	Ser	Ser	Glu	Pro	Glu	Arg	Thr	2565	2570	2575
Asn	Ile	Gln	Asn	Leu	Asn	Gln	Leu	Arg	Glu	Asp	Glu	Leu	Gly	Ser	Asp	2580	2585	2590
Ile	Ser	Ala	Leu	Thr	Leu	Arg	Ile	Ser	Glu	Leu	Glu	Ser	Gln	Val	Val	2595	2600	2605
Glu	Met	His	Thr	Ser	Leu	Ile	Leu	Glu	Lys	Glu	Gln	Val	Glu	Ile	Ala	2610	2615	2620
Glu	Lys	Asn	Val	Leu	Glu	Lys	Glu	Lys	Lys	Leu	Leu	Glu	Leu	Gln	Lys	2625	2630	2635
Leu	Leu	Glu	Gly	Asn	Glu	Lys	Lys	Gln	Arg	Glu	Lys	Glu	Lys	Lys	Arg	2645	2650	2655
Ser	Pro	Gln	Asp	Val	Glu	Val	Leu	Lys	Thr	Thr	Thr	Glu	Leu	Phe	His	2660	2665	2670
Ser	Asn	Glu	Glu	Ser	Gly	Phe	Phe	Asn	Glu	Leu	Glu	Ala	Leu	Arg	Ala	2675	2680	2685
Glu	Ser	Val	Ala	Thr	Lys	Ala	Glu	Leu	Ala	Ser	Tyr	Lys	Glu	Lys	Ala	2690	2695	2700
Glu	Lys	Leu	Gln	Glu	Glu	Leu	Leu	Val	Lys	Glu	Thr	Asn	Met	Thr	Ser	2705	2710	2715
Leu	Gln	Lys	Asp	Leu	Ser	Gln	Val	Arg	Asp	His	Leu	Ala	Glu	Ala	Lys	2720		

2725										2730					2735				
Glu	Lys	Leu	Ser	Ile	Leu	Glu	Lys	Glu	Asp	Glu	Thr	Glu	Val	Gln	Glu				
2740										2745					2750				
Ser	Lys	Lys	Ala	Cys	Met	Phe	Glu	Pro	Leu	Pro	Ile	Lys	Leu	Ser	Lys				
2755										2760					2765				
Ser	Ile	Ala	Ser	Gln	Thr	Asp	Gly	Thr	Leu	Lys	Ile	Ser	Ser	Ser	Asn				
2770										2775					2780				
Gln	Thr	Pro	Gln	Ile	Leu	Val	Lys	Asn	Ala	Gly	Ile	Gln	Ile	Asn	Leu				
2785										2790					2795				
Gln	Ser	Glu	Cys	Ser	Ser	Glu	Glu	Val	Thr	Glu	Ile	Ile	Ser	Gln	Phe				
2805										2810					2815				
Thr	Glu	Lys	Ile	Glu	Lys	Met	Gln	Glu	Leu	His	Ala	Ala	Glu	Ile	Leu				
2820										2825					2830				
Asp	Met	Glu	Ser	Arg	His	Ile	Ser	Glu	Thr	Glu	Thr	Leu	Lys	Arg	Glu				
2835										2840					2845				
His	Tyr	Val	Ala	Val	Gln	Leu	Lys	Glu	Glu	Cys	Gly	Thr	Leu	Lys					
2850										2855					2860				
Ala	Val	Ile	Gln	Cys	Leu	Arg	Ser	Lys	Glu	Gly	Ser	Ser	Ile	Pro	Glu				
2865										2870					2875				
Leu	Ala	His	Ser	Asp	Ala	Tyr	Gln	Thr	Arg	Glu	Ile	Cys	Ser	Ser	Asp				
2885										2890					2895				
Ser	Gly	Ser	Asp	Trp	Gly	Gln	Gly	Ile	Tyr	Leu	Thr	His	Ser	Gln	Gly				
2900										2905					2910				
Phe	Asp	Ile	Ala	Ser	Glu	Gly	Arg	Gly	Glu	Glu	Ser	Glu	Ser	Ala	Thr				
2915										2920					2925				
Asp	Ser	Phe	Pro	Lys	Lys	Ile	Lys	Gly	Leu	Leu	Arg	Ala	Val	His	Asn				
2930										2935					2940				
Glu	Gly	Met	Gln	Val	Leu	Ser	Leu	Thr	Glu	Ser	Pro	Tyr	Ser	Asp	Gly				
2945										2950					2955				
Glu	Asp	His	Ser	Ile	Gln	Gln	Val	Ser	Glu	Pro	Trp	Leu	Glu	Glu	Arg				
2965										2970					2975				
Lys	Ala	Tyr	Ile	Asn	Thr	Ile	Ser	Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys				
2980										2985					2990				
Met	Gln	Leu	Gln	Arg	Glu	Ala	Glu	Val	Tyr	Asp	Ser	Ser	Gln	Ser	His				
2995										3000					3005				
Glu	Ser	Phe	Ser	Asp	Trp	Arg	Gly	Glu	Leu	Leu	Leu	Ala	Leu	Gln	Gln				
3010										3015					3020				
Val	Phe	Leu	Glu	Glu	Arg	Ser	Val	Leu	Leu	Ala	Ala	Phe	Arg	Thr	Glu				
3025										3030					3035				
Leu	Thr	Ala	Leu	Gly	Thr	Thr	Asp	Ala	Val	Gly	Leu	Leu	Asn	Cys	Leu				
3045										3050					3055				
Glu	Gln	Arg	Ile	Gln	Glu	Gln	Gly	Val	Glu	Tyr	Gln	Ala	Ala	Met	Glu				
3060										3065					3070				
Cys	Leu	Gln	Lys	Ala	Asp	Arg	Arg	Ser	Leu	Leu	Ser	Glu	Ile	Gln	Ala				
3075										3080					3085				
Leu	His	Ala	Gln	Met	Asn	Gly	Arg	Lys	Ile	Thr	Leu	Lys	Arg	Glu	Gln				
3090										3095					3100				
Glu	Ser	Glu	Lys	Pro	Ser	Gln	Glu	Leu	Leu	Glu	Tyr	Asn	Ile	Gln	Gln				
3105										3110					3115				
Lys	Gln	Ser	Gln	Met	Leu	Glu	Met	Gln	Val	Glu	Leu	Ser	Ser	Met	Lys				
3125										3130					3135				
Asp	Arg	Ala	Thr	Glu	Leu	Gln	Glu	Gln	Leu	Ser	Ser	Glu	Lys	Met	Val				
3140										3145					3150				
Val	Ala	Glu	Leu	Lys	Ser	Glu	Leu	Ala	Gln	Thr	Lys	Leu	Glu	Leu	Glu				
3155										3160					3165				
Thr	Thr	Leu	Lys	Ala	Gln	His	Lys	His	Leu	Lys	Glu	Leu	Glu	Ala	Phe				
3170										3175					3180				
Arg	Leu	Glu	Val	Lys	Asp	Lys	Thr	Asp	Glu	Val	His	Leu	Leu	Asn	Asp				
3185										3190					3195				
															3200				

Thr Leu Ala Ser. Glu Gln Lys Lys Ser Arg Glu Leu Gln Trp Ala Leu
 3205 3210 3215
 Glu Lys Glu Lys Ala Lys Leu Gly Arg Ser Glu Glu Arg Asp Lys Glu
 3220 3225 3230
 Glu Leu Glu Asp Leu Lys Phe Ser Leu Glu Ser Gln Lys Gln Arg Asn
 3235 3240 3245
 Leu Gln Leu Asn Leu Leu Leu Glu Gln Gln Lys Gln Leu Leu Asn Glu
 3250 3255 3260
 Ser Gln Gln Lys Ile Glu Ser Gln Arg Met Leu Tyr Asp Ala Gln Leu
 3265 3270 3275 3280
 Ser Glu Glu Gln Gly Arg Asn Leu Glu Leu Gln Val Leu Leu Glu Ser
 3285 3290 3295
 Glu Lys Val Arg Ile Arg Glu Met Ser Ser Thr Leu Asp Arg Glu Arg
 3300 3305 3310
 Glu Leu His Ala Gln Leu Gln Ser Ser Asp Gly Thr Gly Gln Ser Arg
 3315 3320 3325
 Pro Pro Leu Pro Ser Glu Asp Leu Leu Lys Glu Leu Gln Lys Gln Leu
 3330 3335 3340
 Glu Glu Lys His Ser Arg Ile Val Glu Leu Leu Asn Glu Thr Glu Lys
 3345 3350 3355 3360
 Tyr Lys Leu Asp Ser Leu Gln Thr Arg Gln Gln Met Glu Lys Asp Arg
 3365 3370 3375
 Gln Val His Arg Lys Thr Leu Gln Thr Glu Gln Glu Ala Asn Thr Glu
 3380 3385 3390
 Gly Gln Lys Lys Met His Glu Leu Gln Ser Lys Val Glu Asp Leu Gln
 3395 3400 3405
 Arg Gln Leu Glu Glu Lys Arg Gln Gln Val Tyr Lys Leu Asp Leu Glu
 3410 3415 3420
 Gly Gln Arg Leu Gln Gly Ile Met Gln Glu Phe Gln Lys Gln Glu Leu
 3425 3430 3435 3440
 Glu Arg Glu Glu Lys Arg Glu Ser Arg Arg Ile Leu Tyr Gln Asn Leu
 3445 3450 3455
 Asn Glu Pro Thr Thr Trp Ser Leu Thr Ser Asp Arg Thr Arg Asn Trp
 3460 3465 3470
 Val Leu Gln Gln Lys Ile Glu Gly Glu Thr Lys Glu Ser Asn Tyr Ala
 3475 3480 3485
 Lys Leu Ile Glu Met Asn Gly Gly Gly Thr Gly Cys Asn His Glu Leu
 3490 3495 3500
 Glu Met Ile Arg Gln Lys Leu Gln Cys Val Ala Ser Lys Leu Gln Val
 3505 3510 3515 3520
 Leu Pro Gln Lys Ala Ser Glu Arg Leu Gln Phe Glu Thr Ala Asp Asp
 3525 3530 3535
 Glu Asp Phe Ile Trp Val Gln Glu Asn Ile Asp Glu Ile Ile Leu Gln
 3540 3545 3550
 Leu Gln Lys Leu Thr Gly Gln Gln Gly Glu Glu Pro Ser Leu Val Ser
 3555 3560 3565
 Pro Ser Thr Ser Cys Gly Ser Leu Thr Glu Arg Leu Leu Arg Gln Asn
 3570 3575 3580
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<212> PRT

<213> Homo sapiens

<400> 6

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Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
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Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
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Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
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Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
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His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
275          280          285
Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
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Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305          310          315          320

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 Asp Ile Val Gln Arg Met Glu Gln Glu Thr Gln Arg Lys Leu Glu Gln
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 Leu Arg Ala Glu Leu Asp Glu Met Tyr Gly Gln Gln Ile Val Gln Met
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 Lys Gln Glu Leu Ile Arg Gln His Met Ala Gln Met Glu Glu Met Lys
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 Thr Arg His Lys Gly Glu Met Glu Asn Ala Leu Arg Ser Tyr Ser Asn
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 Ile Thr Val Asn Glu Asp Gln Ile Lys Leu Met Asn Val Ala Ile Asn
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 Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu

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Lys	Gln	Gln	Cys	Ile	Gln	Leu	Asn	Glu	Glu	Ile	Glu	Lys	Gln	Arg	Asn
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Gln	Glu	Glu	Tyr	Ala	Cys	Leu	Leu	Lys	Val	Lys	Asp	Asp	Leu	Glu	Asp
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	2180	2185
Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu		2190
	2195	2200
		2205

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 Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys Asp
 2245 2250 2255
 Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala Met Ser
 2260 2265 2270
 Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln Ile Ile Gln
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		3150

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<211> 3917

<212> PRT

<213> Homo sapiens

<400> 8

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 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
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His	Gln	Gln	Gln	Leu	Glu	Glu	Gln	Asp	His	Leu	Leu	Glu	Asp	Tyr	Gln	275	280	285
Lys	Lys	Lys	Glu	Asp	Phe	Thr	Met	Gln	Ile	Ser	Phe	Leu	Gln	Glu	Lys	290	295	300
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Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln	355	360	365
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Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr	385	390	400
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr	405	410	415
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Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu	500	505	510
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Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg	610	615	620
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Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys	645	650	655
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn	660	665	670
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu	675	680	685
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp	690	695	700
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln			

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Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu
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Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys
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Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln
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Asn	Glu	Glu	Val	Lys	Ser	Leu	Lys	Gln	Glu	Lys	Glu	Gln	Val	Ser
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Val	Gln	Ser	Cys	Asp	Thr	Gln	Val	Ser	Ser	Leu	Leu	Asp	Gly	Val
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	1925	1930
Gln Ile Gln Glu Lys	Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu	1935
	1940	1945
Leu Cys Ala Ser Asn	Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln	1950
	1955	1960
Ile Gln Glu Glu Arg	Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys	1965
	1970	1975
Ala Glu Ala Gly Pro	Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys	1980
1985	1990	1995
Leu Met Lys Glu Lys	Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg	2000
	2005	2010
Asp Asp Leu Gln Lys	Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu	2015
	2020	2025
Gln Val Ser Arg Phe	Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu	2030
	2035	2040
Met Asp Leu Arg Gln	Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys	2045
	2050	2055
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Asp Val Phe Gln Gln	Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val	2080
	2085	2090
Val Pro Arg Phe Gln	Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu	2095
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	2675	2680
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	2690	2695
Glu Lys Leu Gln Glu Glu Leu Leu Val Lys Glu Thr Asn Met Thr Ser		2700
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Ser Lys Lys Ala Cys Met Phe Glu Pro Leu Pro Ile Lys Leu Ser Lys		2750
	2755	2760
Ser Ile Ala Ser Gln Thr Asp Gly Thr Leu Lys Ile Ser Ser Ser Asn		2765
	2770	2775
Gln Thr Pro Gln Ile Leu Val Lys Asn Ala Gly Ile Gln Ile Asn Leu		2780
2785	2790	2795
Gln Ser Glu Cys Ser Ser Glu Glu Val Thr Glu Ile Ile Ser Gln Phe		2800
	2805	2810
Thr Glu Lys Ile Glu Lys Met Gln Glu Leu His Ala Ala Glu Ile Leu		2815
	2820	2825
Asp Met Glu Ser Arg His Ile Ser Glu Thr Glu Thr Leu Lys Arg Glu		2830
	2835	2840
His Tyr Val Ala Val Gln Leu Leu Lys Glu Glu Cys Gly Thr Leu Lys		2845
	2850	2855
Ala Val Ile Gln Cys Leu Arg Ser Lys Glu Gly Ser Ser Ile Pro Glu		2860
2865	2870	2875
Leu Ala His Ser Asp Ala Tyr Gln Thr Arg Glu Ile Cys Ser Ser Asp		2880
	2885	2890
Ser Gly Ser Asp Trp Gly Gln Gly Ile Tyr Leu Thr His Ser Gln Gly		2895
	2900	2905
Phe Asp Ile Ala Ser Glu Gly Arg Gly Glu Glu Ser Glu Ser Ala Thr		2910
	2915	2920
Asp Ser Phe Pro Lys Lys Ile Lys Gly Leu Leu Arg Ala Val His Asn		2925
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Glu Gly Met Gln Val Leu Ser Leu Thr Glu Ser Pro Tyr Ser Asp Gly		2940
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Glu Asp His Ser Ile Gln Gln Val Ser Glu Pro Trp Leu Glu Glu Arg		2960
	2965	2970
Lys Ala Tyr Ile Asn Thr Ile Ser Ser Leu Lys Asp Leu Ile Thr Lys		2975
	2980	2985
Met Gln Leu Gln Arg Glu Ala Glu Val Tyr Asp Ser Ser Gln Ser His		2990
	2995	3000
Glu Ser Phe Ser Asp Trp Arg Gly Glu Leu Leu Leu Ala Leu Gln Gln		3005
	3010	3015
Val Phe Leu Glu Glu Arg Ser Val Leu Leu Ala Ala Phe Arg Thr Glu		3020
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Leu Thr Ala Leu Gly Thr Thr Asp Ala Val Gly Leu Leu Asn Cys Leu		3040
	3045	3050
Glu Gln Arg Ile Gln Glu Gln Gly Val Glu Tyr Gln Ala Ala Met Glu		3055
	3060	3065
		3070

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 Glu Ser Glu Lys Pro Ser Gln Glu Leu Leu Glu Tyr Asn Ile Gln Gln
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 Lys Gln Ser Gln Met Leu Glu Met Gln Val Glu Leu Ser Ser Met Lys
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 Thr Thr Leu Lys Ala Gln His Lys His Leu Lys Glu Leu Glu Ala Phe
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 Arg Leu Glu Val Lys Asp Lys Thr Asp Glu Val His Leu Leu Asn Asp
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 Lys Leu Ile Glu Met Asn Gly Gly Gly Thr Gly Cys Asn His Glu Leu
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 Glu Asp Phe Ile Trp Val Gln Glu Asn Ile Asp Glu Ile Ile Leu Gln

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3570	3575	3580
Ala Glu Leu Thr Gly His Ile Ser Gln Leu Thr Glu Glu Lys Asn Asp		
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Leu Arg Asn Met Val Met Lys Leu Glu Glu Gln Ile Arg Trp Tyr Arg		
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Gln Thr Gly Ala Gly Arg Asp Asn Ser Ser Arg Phe Ser Leu Asn Gly		
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Gly Ala Asn Ile Glu Ala Ile Ile Ala Ser Glu Lys Glu Val Trp Asn		
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Arg Glu Lys Leu Thr Leu Gln Lys Ser Leu Lys Arg Ala Glu Ala Glu		
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Val Tyr Lys Leu Lys Ala Glu Leu Arg Asn Asp Ser Leu Leu Gln Thr		
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Leu Ser Pro Asp Ser Glu His Val Thr Leu Lys Arg Ile Tyr Gly Lys		
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Tyr Leu Arg Ala Glu Ser Phe Arg Lys Ala Leu Ile Tyr Gln Lys Lys		
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Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr		
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Glu Val Ile Thr Asn Arg Pro Lys Gly Phe Thr Arg Phe Arg Ser Ala		
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Val Arg Val Ser Ile Ala Ile Ser Arg Met Lys Phe Leu Val Arg Arg		
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Trp His Arg Val Thr Gly Ser Val Ser Ile Asn Ile Asn Arg Asp Gly		
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Phe Gly Leu Asn Gln Gly Ala Glu Lys Thr Asp Ser Phe Tyr His Ser		
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3825	3830	3835
Arg Tyr Pro Gly Thr Pro Ala Asp Phe Asn Pro Gly Ser Leu Ala Cys		
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Ser Gln Leu Gln Asn Tyr Asp Pro Asp Arg Ala Leu Thr Asp Tyr Ile		
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Thr Arg Leu Glu Ala Leu Gln Arg Arg Leu Gly Thr Ile Gln Ser Gly		
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Ala Leu Ser Leu Thr Thr Ser Trp Gln His His Ser Ala Arg Pro Thr		
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<211> 2850

<212> DNA

<213> Homo sapiens

<400> 9

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<210> 10

<211> 383

<212> PRT

<213> Homo sapiens

<400> 10

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35           40           45
Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val
50           55           60

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Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn
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Gly Phe Val Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu
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Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys
      100     105     110
Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu
      115     120     125
Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg
      130     135     140
Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala
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Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu
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Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu
      180     185     190
Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile
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Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln
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Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys
225      230     235     240
Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn
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Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg
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Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg
      275     280     285
Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu
      290     295     300
Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu
305      310     315     320
Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr
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Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr
      340     345     350
Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn
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Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
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<210> 11

<211> 3004

<212> DNA

<213> Homo sapiens

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<210> 12

<211> 414

<212> PRT

<213> Homo sapiens

<400> 12

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35          40          45
Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
50          55          60
Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
65          70          75          80
Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
85          90          95

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 180 185 190
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 225 230 235 240
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 260 265 270
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 Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
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 Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
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<210> 13

<211> 2298

<212> DNA

<213> Homo sapiens

<400> 13

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<211> 331

<212> PRT

<213> Homo sapiens

<400> 14

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Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
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Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
65        70        75        80
Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
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Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
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Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
115       120       125
Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
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145       150       155       160
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Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
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Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
    260                265                270
Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
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Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
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<212> DNA
<213> Homo sapiens

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<210> 16
<211> 265
<212> PRT
<213> Homo sapiens

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Glu Phe Leu Ala Thr Leu Ile Phe Val Phe Phe Gly Leu Gly Ser Ala
    20              25              30

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	50					55					60				
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	65				70					75					80
Gln	Ile	Ser	Leu	Leu	Arg	Ala	Phe	Phe	Tyr	Val	Ala	Ala	Gln	Leu	Val
				85					90					95	
Gly	Ala	Ile	Ala	Gly	Ala	Gly	Ile	Leu	Tyr	Gly	Val	Ala	Pro	Leu	Asn
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Ala	Arg	Gly	Asn	Leu	Ala	Val	Asn	Ala	Leu	Asn	Asn	Asn	Thr	Thr	Gln
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Gly	Gln	Ala	Met	Val	Val	Glu	Leu	Ile	Leu	Thr	Phe	Gln	Leu	Ala	Leu
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Cys	Ile	Phe	Ala	Ser	Thr	Asp	Ser	Arg	Arg	Thr	Ser	Pro	Val	Gly	Ser
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Pro	Ala	Leu	Ser	Ile	Gly	Leu	Ser	Val	Thr	Leu	Gly	His	Leu	Val	Gly
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Ile	Tyr	Phe	Thr	Gly	Cys	Ser	Met	Asn	Pro	Ala	Arg	Ser	Phe	Gly	Pro
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	210					215					220				
Leu	Phe	Pro	Asn	Ser	Leu	Ser	Leu	Ser	Glu	Arg	Val	Ala	Ile	Ile	Lys
	225				230				235						240
Gly	Thr	Tyr	Glu	Pro	Asp	Glu	Asp	Trp	Glu	Glu	Gln	Arg	Glu	Glu	Arg
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<211> 1258

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18
 <211> 22
 <212> PRT
 <213> Homo sapiens

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 Lys Leu Phe Asp Ser Tyr
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<210> 19
 <211> 983
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 20 25 30
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 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
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<210> 21

<211> 4859

<212> DNA

<213> Homo sapiens

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<210> 22

<211> 244

<212> PRT

<213> Homo sapiens

<400> 22

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20          25          30
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35          40          45
Asp Pro Gly Asp Thr Trp Lys Asp Tyr Cys Thr Leu Val Thr Ile Ala
50          55          60
Lys Ser Leu Leu Asp Leu Asn Lys Tyr Arg Pro Ile Gln Thr Pro Ser
65          70          75          80
Val Cys Ser Asp Ser Leu Glu Ser Pro Asp Glu Asp Met Gly Ser Asp
85          90          95
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 Cys Pro Tyr Ser Gly Cys Gly Lys Val Tyr Gly Lys Ser Ser His Leu
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 Lys Ala His Tyr Arg Val His Thr Gly Glu Arg Pro Phe Pro Cys Thr
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 Trp Pro Asp Cys Leu Lys Lys Phe Ser Arg Ser Asp Glu Leu Thr Arg
 180 185 190
 His Tyr Arg Thr His Thr Gly Glu Lys Gln Phe Arg Cys Pro Leu Cys
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Ala	Thr	Thr	Ala	Tyr	Phe	Leu	Tyr	Gln	Gln	Gln	Gly	Arg	Leu	Asp	Lys
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Leu	Thr	Val	Thr	Ser	Gln	Asn	Leu	Gln	Leu	Glu	Asn	Leu	Arg	Met	Lys
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Leu	Pro	Lys	Pro	Pro	Lys	Pro	Val	Ser	Lys	Met	Arg	Met	Ala	Thr	Pro
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Glu	Ser	Leu	Glu	Leu	Glu	Asp	Pro	Ser	Ser	Gly	Leu	Gly	Val	Thr	Lys
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<211> 1615

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens
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Pro	His	Arg	Ser	Ala	Ala	Gln	Met	Glu	Val	Ala	Ser	Phe	Leu	Leu	Ser
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Lys	Glu	Asn	Gln	Pro	Glu	Asn	Ser	Gln	Thr	Pro	Thr	Lys	Lys	Glu	His
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Gly	Arg	His	Leu	Ala	Ser	Gly	Gly	Asn	Asp	Asn	Leu	Val	Asn	Val	Trp
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<211> 2103

<212> DNA

<213> Homo sapiens

<400> 27

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 <212> PRT
 <213> Homo sapiens

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 Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala
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 Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys
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 Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser
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<210> 30

<211> 184

<212> PRT

<213> Homo sapiens

<400> 30

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Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln
 35           40           45
Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg

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Leu His Val Thr	Glu Arg Lys Tyr Leu Lys Arg	Asp Trp Cys Lys Thr		
	85	90	95	
Gln Pro Leu Lys	Gln Thr Ile His Glu Glu Gly	Cys Asn Ser Arg Thr		
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Ile Ile Asn Arg	Phe Cys Tyr Gly Gln Cys Asn	Ser Phe Tyr Ile Pro		
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Arg His Ile Arg	Lys Glu Glu Gly Ser Phe Gln	Ser Cys Ser Phe Cys		
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Lys Pro Lys Lys	Phe Thr Thr Met Met Val Thr	Leu Asn Cys Pro Glu		
145	150	155	160	
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<210> 31

<211> 3443

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32

<211> 211

<212> PRT

<213> Homo sapiens

<400> 32

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          20          25          30
Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala Met Tyr Glu
          35          40          45
Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly Gln Ile Gln Cys
          50          55          60
Lys Val Phe Asp Ser Leu Asn Leu Ser Ser Thr Leu Gln Ala Thr
          65          70          75          80
Arg Ala Leu Met Val Val Gly Ile Leu Leu Gly Val Ile Ala Ile Phe
          85          90          95
Val Ala Thr Val Gly Met Lys Cys Met Lys Cys Leu Glu Asp Asp Glu
          100          105          110
Val Gln Lys Met Arg Met Ala Val Ile Gly Gly Ala Ile Phe Leu Leu
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Ala Gly Leu Ala Ile Leu Val Ala Thr Ala Trp Tyr Gly Asn Arg Ile
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Phe Gly Gln Ala Leu Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu
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<210> 33
 <211> 4318
 <212> DNA
 <213> Homo sapiens

<400> 33

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<210> 34

<211> 253

<212> PRT

<213> Homo sapiens

<400> 34

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35     40     45
Gly Val Val Phe Ser Val Thr Val Asp Leu Lys Arg Lys Pro Ala
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Asp Leu Gln Asn Leu Ala Pro Gly Thr His Pro Pro Phe Ile Thr Phe
65     70     75     80
Asn Ser Glu Val Lys Thr Asp Val Asn Lys Ile Glu Glu Phe Leu Glu
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Glu Val Leu Cys Pro Pro Lys Tyr Leu Lys Leu Ser Pro Lys His Pro
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<212> DNA
<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Tyr	Asp Glu Tyr Lys Lys	Gly Phe Leu Asp Gln	Ala Ser Gly Ser Ala		
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<212> DNA

<213> Homo sapiens

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<211> 1224

<212> PRT

<213> Homo sapiens

<400> 42

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Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
 50          55          60
Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
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Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
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Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
100          105          110
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Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
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Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
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Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr
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305          310          315          320
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<211> 266

<212> DNA

<213> Homo sapiens

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<210> 46

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<212> PRT

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 20          25          30
Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35          40          45
Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50          55          60
Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65          70          75          80
Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85          90          95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100          105          110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115          120          125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130          135          140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145          150          155          160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165          170          175
Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180          185          190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195          200          205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210          215          220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225          230          235          240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245          250          255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260          265          270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275          280          285
Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
290          295          300
Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305          310          315          320
Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
325          330          335
Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
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<210> 47
 <211> 3025
 <212> DNA
 <213> Homo sapiens

<400> 47

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<210> 48

<211> 752

<212> PRT

<213> Homo sapiens

<400> 48

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 20          25          30
Lys Leu Ala Leu Ala Glu Ala Arg Val Gln Glu Glu Gln Lys Ala
 35          40          45
Thr Arg Leu Glu Lys Glu Leu Gln Thr Gln Thr Thr Lys Phe His Gln
 50          55          60
Asp Gln Asp Thr Ile Met Ala Lys Leu Thr Asn Glu Asp Ser Gln Asn
 65          70          75          80
Arg Gln Leu Gln Gln Lys Leu Ala Ala Leu Ser Arg Gln Ile Asp Glu
 85          90          95
Leu Glu Glu Thr Asn Arg Ser Leu Arg Lys Ala Glu Glu Glu Leu Gln
100          105          110
Asp Ile Lys Glu Lys Ile Ser Lys Gly Glu Tyr Gly Asn Ala Gly Ile
115          120          125
Met Ala Glu Val Glu Glu Leu Ile Lys Met Glu Glu Gln Cys Arg Asp
130          135          140
Leu Asn Lys Arg Leu Glu Arg Glu Thr Leu Gln Ser Lys Asp Phe Lys
145          150          155          160
Leu Glu Val Glu Lys Leu Ser Lys Arg Ile Met Ala Leu Glu Lys Leu
165          170          175
Glu Asp Ala Phe Asn Lys Ser Lys Gln Glu Cys Tyr Ser Leu Lys Cys
180          185          190
Asn Leu Glu Lys Glu Arg Met Thr Thr Lys Gln Leu Ser Gln Glu Leu
195          200          205
Glu Ser Leu Lys Val Arg Ile Lys Glu Leu Glu Ala Ile Glu Ser Arg
210          215          220
Leu Glu Lys Thr Glu Phe Thr Leu Lys Glu Asp Leu Thr Lys Leu Lys
225          230          235          240
Thr Leu Thr Val Met Phe Val Asp Glu Arg Lys Thr Met Ser Glu Lys
245          250          255
Leu Lys Lys Thr Glu Asp Lys Leu Gln Ala Ala Ser Ser Gln Leu Gln
260          265          270
Val Glu Gln Asn Lys Val Thr Thr Val Thr Glu Lys Leu Ile Glu Glu
275          280          285
Thr Lys Arg Ala Leu Lys Ser Lys Thr Asp Val Glu Glu Lys Met Tyr
290          295          300
Ser Val Thr Lys Glu Arg Asp Asp Leu Lys Asn Lys Leu Lys Ala Glu
305          310          315          320
Glu Glu Lys Gly Asn Asp Leu Leu Ser Arg Val Asn Met Leu Lys Asn
325          330          335
Arg Leu Gln Ser Leu Glu Ala Ile Glu Lys Asp Phe Leu Lys Asn Lys
340          345          350
Leu Asn Gln Asp Ser Gly Lys Ser Thr Thr Ala Leu His Gln Glu Asn
355          360          365
Asn Lys Ile Lys Glu Leu Ser Gln Glu Val Glu Arg Leu Lys Leu Lys
370          375          380
Leu Lys Asp Met Lys Ala Ile Glu Asp Asp Leu Met Lys Thr Glu Asp
385          390          395          400
Glu Tyr Glu Thr Leu Glu Arg Arg Tyr Ala Asn Glu Arg Asp Lys Ala
405          410          415
Gln Phe Leu Ser Lys Glu Leu Glu His Val Lys Met Glu Leu Ala Lys
420          425          430

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Tyr	Lys	Leu	Ala	Glu	Lys	Thr	Glu	Thr	Ser	His	Glu	Gln	Trp	Leu	Phe
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Lys	Arg	Leu	Gln	Glu	Glu	Glu	Ala	Lys	Ser	Gly	His	Leu	Ser	Arg	Glu
	450					455					460				
Val	Asp	Ala	Leu	Lys	Glu	Lys	Ile	His	Glu	Tyr	Met	Ala	Thr	Glu	Asp
	465				470					475					480
Leu	Ile	Cys	His	Leu	Gln	Gly	Asp	His	Ser	Val	Cys	Lys	Lys	Lys	Leu
				485					490					495	
Asn	Gln	Gln	Glu	Asn	Arg	Asn	Arg	Asp	Leu	Gly	Arg	Glu	Ile	Glu	Asn
			500					505					510		
Leu	Thr	Lys	Glu	Leu	Glu	Arg	Tyr	Arg	His	Phe	Ser	Lys	Ser	Leu	Arg
		515					520					525			
Pro	Ser	Leu	Asn	Gly	Arg	Arg	Ile	Ser	Asp	Pro	Gln	Val	Phe	Ser	Lys
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Glu	Val	Gln	Thr	Glu	Ala	Val	Asp	Asn	Glu	Pro	Pro	Asp	Tyr	Lys	Ser
	545				550					555					560
Leu	Ile	Pro	Leu	Glu	Arg	Ala	Val	Ile	Asn	Gly	Gln	Leu	Tyr	Glu	Glu
				565					570					575	
Ser	Glu	Asn	Gln	Asp	Glu	Asp	Pro	Asn	Asp	Glu	Gly	Ser	Val	Leu	Ser
			580						585				590		
Phe	Lys	Cys	Ser	Gln	Ser	Thr	Pro	Cys	Pro	Val	Asn	Arg	Lys	Leu	Trp
	595						600					605			
Ile	Pro	Trp	Met	Lys	Ser	Lys	Glu	Gly	His	Leu	Gln	Asn	Gly	Lys	Met
	610					615					620				
Gln	Thr	Lys	Pro	Asn	Ala	Asn	Phe	Val	Gln	Pro	Gly	Asp	Leu	Val	Leu
	625				630					635					640
Ser	His	Thr	Pro	Gly	Gln	Pro	Leu	His	Ile	Lys	Val	Thr	Pro	Asp	His
				645					650					655	
Val	Gln	Asn	Thr	Ala	Thr	Leu	Glu	Ile	Thr	Ser	Pro	Thr	Thr	Glu	Ser
			660					665					670		
Pro	His	Ser	Tyr	Thr	Ser	Thr	Ala	Val	Ile	Pro	Asn	Cys	Gly	Thr	Pro
		675					680					685			
Lys	Gln	Arg	Ile	Thr	Ile	Leu	Gln	Asn	Ala	Ser	Ile	Thr	Pro	Val	Lys
	690					695					700				
Ser	Lys	Thr	Ser	Thr	Glu	Asp	Leu	Met	Asn	Leu	Glu	Gln	Gly	Met	Ser
	705				710					715					720
Pro	Ile	Thr	Met	Ala	Thr	Phe	Ala	Arg	Ala	Gln	Thr	Pro	Glu	Ser	Cys
			725					730						735	
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<210> 49

<211> 1480

<212> DNA

<213> Homo sapiens

<400> 49

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<210> 50

<211> 205

<212> PRT

<213> Homo sapiens

<400> 50

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20     25     30
Arg Asn Glu Asp Tyr Thr Ile His Val Gln Leu Asn Asp Tyr Val Asp
35     40     45
Ile Ile Cys Pro His Tyr Glu Asp His Ser Val Ala Asp Ala Ala Met
50     55     60
Glu Gln Tyr Ile Leu Tyr Leu Val Glu His Glu Tyr Gln Leu Cys
65     70     75     80
Gln Pro Gln Ser Lys Asp Gln Val Arg Trp Gln Cys Asn Arg Pro Ser
85     90     95
Ala Lys His Gly Pro Glu Lys Leu Ser Glu Lys Phe Gln Arg Phe Thr
100    105    110
Pro Phe Thr Leu Gly Lys Glu Phe Lys Glu Gly His Ser Tyr Tyr Tyr
115    120    125
Ile Ser Lys Pro Ile His Gln His Glu Asp Arg Cys Leu Arg Leu Lys
130    135    140
Val Thr Val Ser Gly Lys Ile Thr His Ser Pro Gln Ala His Val Asn
145    150    155    160
Pro Gln Glu Lys Arg Leu Ala Ala Asp Asp Pro Glu Val Arg Val Leu
165    170    175
His Ser Ile Gly His Ser Ala Ala Pro Arg Leu Phe Pro Leu Ala Trp
180    185    190
Thr Val Leu Leu Leu Pro Leu Leu Leu Leu Gln Thr Pro
195    200    205

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<210> 51

<211> 15952

<212> DNA

<213> Homo sapiens

<400> 51

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tttactagga aaaattctga acaagtaaaa tatgaaggaa aaaaaaaaaa aa 15952

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<211> 5065

<212> PRT

<213> Homo sapiens

<400> 52

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20 25 30
Tyr Ala Ala Met Glu Gln Gly Leu Leu Pro Ala Gly Leu Gly Gln Ala
35 40 45
Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Leu Val Asp Leu Ala Arg
50 55 60
Gly Gln Leu Leu Pro Val Ser Lys Ala Leu Gln Gln Gly Leu Val Gly
65 70 75 80
Leu Glu Leu Lys Glu Lys Leu Leu Ala Ala Glu Arg Ala Thr Thr Gly
85 90 95
Tyr Pro Asp Pro Tyr Gly Gly Glu Lys Leu Ala Leu Phe Gln Ala Ile
100 105 110
Gly Lys Glu Val Val Asp Arg Ala Leu Gly Gln Ser Trp Leu Glu Val
115 120 125
Gln Leu Ala Thr Gly Gly Leu Val Asp Pro Ala Gln Gly Val Leu Val
130 135 140
Ala Pro Glu Pro Ala Cys His Gln Gly Leu Leu Asp Arg Glu Thr Trp
145 150 155 160
His Lys Leu Ser Glu Leu Glu Pro Gly Thr Gly Asp Leu Arg Phe Leu
165 170 175
Asn Pro Asn Thr Leu Glu Arg Leu Thr Tyr His Gln Leu Leu Glu Arg
180 185 190
Cys Val Arg Ala Pro Gly Ser Gly Leu Ala Leu Leu Pro Leu Lys Ile
195 200 205

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Thr	Phe	Arg	Ser	Met	Gly	Gly	Ala	Val	Ser	Ala	Ala	Glu	Leu	Leu	Glu
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Val	Gly	Ile	Leu	Asp	Glu	Gln	Ala	Val	Gln	Gly	Leu	Arg	Glu	Gly	Arg
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Leu	Ala	Ala	Val	Asp	Val	Ser	Ala	Arg	Ala	Glu	Val	Arg	Arg	Tyr	Leu
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Glu	Gly	Thr	Gly	Ser	Val	Ala	Gly	Val	Val	Leu	Leu	Pro	Glu	Gly	His
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Lys	Lys	Ser	Phe	Phe	Gln	Ala	Ala	Thr	Glu	His	Leu	Leu	Pro	Met	Gly
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Asp	Pro	Ile	Thr	Gly	Gln	Arg	Leu	Trp	Val	Asp	Glu	Ala	Val	Arg	Ala
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Gly	Leu	Val	Ser	Pro	Glu	Leu	His	Glu	Gln	Leu	Leu	Val	Ala	Glu	Gln
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Ala	Val	Thr	Gly	His	His	Asp	Pro	Phe	Ser	Gly	Ser	Gln	Ile	Pro	Leu
			340					345					350		
Phe	Gln	Ala	Met	Lys	Lys	Gly	Leu	Val	Asp	Arg	Pro	Leu	Ala	Leu	Arg
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Leu	Leu	Asp	Ala	Gln	Leu	Ala	Thr	Gly	Gly	Leu	Val	Cys	Pro	Ala	Arg
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Glu	Asp	Thr	Gln	Arg	Gln	Leu	Ser	Gln	Ala	Gly	Ser	Phe	Ser	Asp	Gly
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Ala	Leu	Ser	Thr	Ala	Thr	Ala	Thr	Val	Ser	Val	Gly	Lys	Phe	Arg	Gly
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Arg	Pro	Val	Ser	Leu	Trp	Glu	Leu	Leu	Phe	Ser	Glu	Ala	Ile	Ser	Ser
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Glu	Gln	Arg	Ala	Met	Leu	Ala	Gln	Gln	Tyr	Gln	Glu	Gly	Thr	Leu	Ser
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Val	Glu	Lys	Leu	Ala	Ala	Glu	Leu	Ser	Ala	Thr	Leu	Glu	Gln	Ala	Ala
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Gly	Glu	Leu	Leu	Lys	Ala	Glu	Ile	Ile	Asp	Gln	Asp	Leu	Tyr	Glu	Arg
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Leu	Glu	His	Gly	Gln	Ala	Thr	Ala	Lys	Asp	Val	Gly	Ser	Leu	Ala	Ser
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Thr	Gly	Phe	Ile	Ile	Asp	Pro	Lys	Ala	Asn	Lys	Gly	His	Ser	Val	Glu
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Glu	Ala	Leu	Arg	Ala	Ala	Val	Ile	Gly	Pro	Asp	Val	Phe	Ala	Lys	Leu
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Leu	Ser	Ala	Glu	Arg	Ala	Val	Thr	Gly	Tyr	Thr	Asp	Pro	Tyr	Thr	Gly
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Gln	Gln	Ile	Ser	Leu	Phe	Gln	Ala	Met	Gln	Lys	Gly	Leu	Ile	Val	Arg

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Ile Asp Pro Val His Ser	His Arg Val Pro Val Asp	Val Ala Tyr Arg
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Arg Gly Tyr Phe Asp Gln	Met Leu Asn Leu Ile Leu	Leu Asp Pro Ser
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Tyr Leu Leu Pro Leu Ser	Ser Thr Gln Ser Pro Leu	Val Asp Ser Ala
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His Gln Leu Leu Glu Ala	Gly Ile Ile Asp Gln Gln	Leu Leu Asp Gln
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Glu Ala Val Arg Arg Gly	Val Val Gly Pro Glu Leu	Tyr Gly Arg Leu
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Glu Gln Ala Ala Arg Leu	Leu Glu Ala Gln Val Ala	Thr Gly Gly Ile
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 Thr Gln Ser Pro Ala Gln Val Ala Glu Gln Pro Ala Val Lys Ala Cys
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 His Gly Val His Leu Pro Gln Ala Ala Ala Cys Arg Leu Gly Leu Leu
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 Lys Arg Arg Glu Leu Val Ala Leu Cys Arg Ser Gly Arg Ala Ala Ala
 1460 1465 1470
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Cys	Ile	Ala	Gly	Val	Thr
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His	Glu	Ala	Ser	Arg	Lys
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Arg	Gln	Lys	Leu	Ser	Val
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Glu	Glu	Leu	Arg	Glu	Arg
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Tyr	Arg	Asp	Pro	Ala	Thr
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Gln	Lys	Gln	Leu	Ile	Glu
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Gln	Val	Ala	Thr	Gly	Gly
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Arg	Asp	Ser	Glu	His	Ile
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 Arg Tyr Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala
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 Lys Asp Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met
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 Gln Ala Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu
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 Ser Val Glu Glu Pro Val Pro Ala Gly Val Val Gly Ser Glu Ile Gln
 2260 2265 2270
 Glu Lys Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro
 2275 2280 2285
 Tyr Thr Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu
 2290 2295 2300
 Ile Val Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr
 2305 2310 2315 2320
 Gly Gly Val Ile Asp Pro Val His Ser His Arg Val Pro Val Asp Val
 2325 2330 2335
 Ala Tyr Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala
 2340 2345 2350
 Asp Pro Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu
 2355 2360 2365
 Asn Leu Thr Tyr Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp
 2370 2375 2380
 Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His
 2385 2390 2395 2400
 Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr
 2405 2410 2415
 Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu
 2420 2425 2430
 Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser
 2435 2440 2445
 Arg Tyr Arg Ala Gly Thr Leu Thr Val Glu Glu Leu Gly Ala Thr Leu
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 Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln Ala Arg Ala Glu Ala Glu
 2465 2470 2475 2480
 Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu Ala Leu Arg Ala Ala Thr
 2485 2490 2495
 Met Glu Val Lys Val Gly Arg Leu Arg Gly Arg Ala Val Pro Val Trp
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 Pro Gln Leu Gln Asp Ala Arg Arg Gly Pro Arg Glu Pro Gly Pro Ala

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Gln	Val	Ser	Ala	Ser	Glu	Leu	His	Thr	Ser	Gly	Ile	Leu	Gly	Pro	Glu										
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Met	Asn	Arg	Val	Leu	Ala	Asp	Pro	Ser	Asp	Asp	Thr	Lys	Gly	Phe	Phe										
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Glu	Leu	Gly	Ala	Thr	Leu	Thr	Ser	Leu	Leu	Ala	Gln	Ala	Gln	Ala	Gln										
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																				3040					

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 3140 3145 3150
 Glu Val Gln Arg Gly Gln Phe Gln Gly Arg Pro Val Ser Val Trp Asp
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 Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu
 3170 3175 3180
 Ala Gln His Ala Ala Gly Ala Leu Gly Leu Pro Asp Leu Val Ala Val
 3185 3190 3195 3200
 Leu Thr Arg Val Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys Val Ser
 3205 3210 3215
 Phe Arg Gly Leu Arg Arg Gln Val Ser Ala Ser Glu Leu His Thr Ser
 3220 3225 3230
 Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys
 3235 3240 3245
 Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr Leu Glu
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 Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala Lys Asp Gln Pro
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 His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile
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 Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr
 3425 3430 3435 3440
 Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr
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 Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His Gln Leu Ser Glu
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 Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr Pro Gly Ser Gly
 3475 3480 3485
 Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu Leu Phe Tyr Arg
 3490 3495 3500
 Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala

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Arg Pro Asp Pro	Arg Glu Ala Leu Arg	Ala Ala Thr Met	Glu Val Lys			
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Val Gly Arg Leu	Arg Gly Arg Ala	Val Pro Val Trp	Asp Val Leu Ala			
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Ser Gly Tyr Val	Ser Gly Ala Ala	Arg Glu Glu Leu	Ala Glu Phe			
3585	3590	3595	3600			
Gly Ser Gly Thr	Leu Asp Leu Pro	Ala Leu Thr Arg	Arg Leu Thr Ala			
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Ile Ile Glu Glu	Ala Glu Glu Ala	Pro Gly Ala Arg	Pro Gln Leu Gln			
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Asp Ala Trp Arg	Gly Pro Arg Glu	Pro Gly Pro Ala	Gly Arg Gly Asp			
	3635	3640	3645			
Gly Asp Ser Gly	Arg Ser Gln Arg	Glu Gly Gln Gly	Glu Gly Glu Thr			
	3650	3655	3660			
Gln Glu Ala Ala	Ala Ala Ala Ala	Ala Ala Arg Arg	Gln Glu Gln Thr			
3665	3670	3675	3680			
Leu Arg Asp Ala	Thr Met Glu Val	Gln Arg Gly Gln	Phe Gln Gly Arg			
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Pro Val Ser Val	Trp Asp Val Leu	Phe Ser Ser Tyr	Leu Ser Glu Ala			
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Arg Arg Asp Glu	Leu Leu Ala Gln	His Ala Ala Gly	Ala Leu Gly Leu			
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Leu Ala Gln Gly	Thr Lys Thr Leu	Gln Glu Val Thr	Glu Met Asp Ser			
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Val Lys Arg Tyr	Leu Glu Gly Thr	Ser Cys Ile Ala	Gly Val Leu Val			
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Arg Leu Ser Val	Glu Glu Ala Val	Ala Ala Gly Val	Val Gly Gly Glu			
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Asp Pro Tyr Thr	Gly Gln Gln Ile	Ser Leu Phe Gln	Ala Met Gln Lys			
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Ala Thr Gly Gly	Val Ile Asp Pro	Val His Ser His	Arg Val Pro Val			
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Asp Val Ala Tyr	Arg Arg Gly Tyr	Phe Asp Glu Glu	Met Asn Arg Val			
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Leu Ala Asp Pro	Ser Asp Asp Thr	Lys Gly Phe Phe	Asp Pro Asn Thr			
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His Glu Asn Leu	Thr Tyr Val Gln	Leu Leu Arg Arg	Cys Val Pro Asp			
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 Val Trp Asp Val Leu Ala Ser Gly Tyr Val Ser Arg Ala Ala Arg Glu
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 4435 4440 4445
 Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile Asp Pro Val His

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	4500	4505
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	4530	4535
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	4580	4585
Val Glu Glu Leu Gly Ala Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln		4590
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Ser Gly Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr		4655
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	4675	4680
Ala Glu Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg		4685
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Thr Lys Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr		4845
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Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met Trp Lys		4880
	4885	4890
Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala		4895
	4900	4905
Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu Ser Val		4910
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		4925

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 <213> Homo sapiens

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 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 54

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Thr Glu Phe Pro Glu Leu Ala Pro Ser Gln Asn Gln Asn His Leu Lys
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Asp Trp Phe Leu Glu Asn Lys Ser Glu Val Cys Glu Cys Arg Asn Asn
          50          55          60
Glu Asp Gly Pro Gly Leu Ile Met Glu Glu Gln His Lys Cys Ser Ser
          65          70          75          80
Lys Ser Leu Glu His Lys Thr Gln Thr Pro Pro Val Glu Glu Asn Val
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Thr Gln Lys Ile Ser Asp Leu Glu Ile Cys Ala Asp Glu Phe Pro Gly
          100          105          110
Ser Ser Ala Thr Tyr Arg Ile Leu Glu Val Gly Cys Gly Val Gly Asn
          115          120          125
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          130          135          140
Tyr Cys Cys Asp Phe Ser Ser Thr Ala Ile Glu Leu Val Gln Thr Asn
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Ser Glu Tyr Asp Pro Ser Arg Cys Phe Ala Phe Val His Asp Leu Cys
          165          170          175
Asp Glu Glu Lys Ser Tyr Pro Val Pro Lys Gly Ser Leu Asp Ile Ile
          180          185          190
Ile Leu Ile Phe Val Leu Ser Ala Ile Val Pro Asp Lys Met Gln Lys
          195          200          205
Ala Ile Asn Arg Leu Ser Arg Leu Leu Lys Pro Gly Gly Met Val Leu
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Leu Arg Asp Tyr Gly Arg Tyr Asp Met Ala Gln Leu Arg Phe Lys Lys
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Val Tyr Phe Phe Thr Gln Glu Glu Leu Asp Thr Leu Phe Thr Thr Ala
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Gly Leu Glu Lys Val Gln Asn Leu Val Asp Arg Arg Leu Gln Val Asn
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<211> 3334

<212> DNA

<213> Homo sapiens

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 <211> 509
 <212> PRT
 <213> Homo sapiens

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<210> 58
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 58
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 Ala Trp Gly Ser Ala Thr Arg Glu Gly Phe Asp Arg Ser Thr Ser
 35 40 45
 Leu Glu Ser Ser Asp Cys Glu Ser Leu Asp Ser Ser Asn Ser Gly Phe
 50 55 60
 Gly Pro Glu Glu Asp Thr Ala Tyr Leu Asp Gly Val Ser Leu Pro Asp
 65 70 75 80
 Phe Glu Leu Leu Ser Asp Pro Glu Asp Glu His Leu Cys Ala Asn Leu
 85 90 95
 Met Gln Leu Leu Gln Glu Ser Leu Ala Gln Ala Arg Leu Gly Ser Arg
 100 105 110

Arg	Pro	Ala	Arg	Leu	Leu	Met	Pro	Ser	Gln	Leu	Val	Ser	Gln	Val	Gly
	115						120					125			
Lys	Glu	Leu	Leu	Arg	Leu	Ala	Tyr	Ser	Glu	Pro	Cys	Gly	Leu	Arg	Gly
	130					135					140				
Ala	Leu	Leu	Asp	Val	Cys	Val	Glu	Gln	Gly	Lys	Ser	Cys	His	Ser	Val
145					150					155					160
Gly	Gln	Leu	Ala	Leu	Asp	Pro	Ser	Leu	Val	Pro	Thr	Phe	Gln	Leu	Thr
			165						170					175	
Leu	Val	Leu	Arg	Leu	Asp	Ser	Arg	Leu	Trp	Pro	Lys	Ile	Gln	Gly	Leu
		180						185					190		
Phe	Ser	Ser	Ala	Asn	Ser	Pro	Phe	Leu	Pro	Gly	Phe	Ser	Gln	Ser	Leu
	195					200						205			
Thr	Leu	Ser	Thr	Gly	Phe	Arg	Val	Ile	Lys	Lys	Lys	Leu	Tyr	Ser	Ser
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Glu	Gln	Leu	Leu	Ile	Glu	Glu	Cys								
225					230										

<210> 59

<211> 2012

<212> DNA

<213> Homo sapiens

<400> 59

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gacatctcag	agtagagggt	ggaatgggga	gaagatgaag	aatccttaga	actcatttat	600
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caggctataa	atgaaattgg	agctggacca	tttagtcagt	tcattaaagc	aaaaactcgg	1020
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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aa			2012

<210> 60
 <211> 495
 <212> PRT
 <213> Homo sapiens

<400> 60

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			20					25					30		
Arg	Val	Arg	Ala	Leu	Asn	Asp	Gly	Gly	Tyr	Gly	Pro	Tyr	Ser	Asp	Val
		35					40					45			
Ser	Glu	Ile	Thr	Thr	Ala	Ala	Gly	Pro	Pro	Gly	Gln	Cys	Lys	Ala	Pro
	50					55					60				
Cys	Ile	Ser	Cys	Thr	Pro	Asp	Gly	Cys	Val	Leu	Val	Gly	Trp	Glu	Ser
65					70					75				80	
Pro	Asp	Ser	Ser	Gly	Ala	Asp	Ile	Ser	Glu	Tyr	Arg	Leu	Glu	Trp	Gly
				85					90					95	
Glu	Asp	Glu	Glu	Ser	Leu	Glu	Leu	Ile	Tyr	His	Gly	Thr	Asp	Thr	Arg
			100					105					110		
Phe	Glu	Ile	Arg	Asp	Leu	Leu	Pro	Ala	Ala	Gln	Tyr	Cys	Cys	Arg	Leu
		115					120					125			
Gln	Ala	Phe	Asn	Gln	Ala	Gly	Ala	Gly	Pro	Tyr	Ser	Glu	Leu	Val	Leu
	130					135					140				
Cys	Gln	Thr	Pro	Ala	Ser	Ala	Pro	Asp	Pro	Val	Ser	Thr	Leu	Cys	Val
145					150					155				160	
Leu	Glu	Glu	Glu	Pro	Leu	Asp	Ala	Tyr	Pro	Asp	Ser	Pro	Ser	Ala	Cys
				165					170					175	
Leu	Val	Leu	Asn	Trp	Glu	Glu	Pro	Cys	Asn	Asn	Gly	Ser	Glu	Ile	Leu
			180					185					190		
Ala	Tyr	Thr	Ile	Asp	Leu	Gly	Asp	Thr	Ser	Ile	Thr	Val	Gly	Asn	Thr
		195					200					205			
Thr	Met	His	Val	Met	Lys	Asp	Leu	Leu	Pro	Glu	Thr	Thr	Tyr	Arg	Ile
	210					215					220				
Arg	Ile	Gln	Ala	Ile	Asn	Glu	Ile	Gly	Ala	Gly	Pro	Phe	Ser	Gln	Phe
225					230					235				240	
Ile	Lys	Ala	Lys	Thr	Arg	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Arg	Leu	Glu
				245					250					255	
Cys	Ala	Ala	Ala	Gly	Pro	Gln	Ser	Leu	Lys	Leu	Lys	Trp	Gly	Asp	Ser
			260					265					270		
Asn	Ser	Lys	Thr	His	Ala	Ala	Glu	Asp	Ile	Val	Tyr	Thr	Leu	Gln	Leu
		275					280					285			
Glu	Asp	Arg	Asn	Lys	Arg	Phe	Ile	Ser	Ile	Tyr	Arg	Gly	Pro	Ser	His
	290					295					300				
Thr	Tyr	Lys	Val	Gln	Arg	Leu	Thr	Glu	Phe	Thr	Cys	Tyr	Ser	Phe	Arg
305					310					315				320	
Ile	Gln	Ala	Ala	Ser	Glu	Ala	Gly	Glu	Gly	Pro	Phe	Ser	Glu	Thr	Tyr
				325					330					335	
Thr	Phe	Ser	Thr	Thr	Lys	Ser	Val	Pro	Pro	Thr	Ile	Lys	Ala	Pro	Arg
			340					345					350		
Val	Thr	Gln	Leu	Glu	Gly	Asn	Ser	Cys	Glu	Ile	Leu	Trp	Glu	Thr	Val
			355				360					365			
Pro	Ser	Met	Lys	Gly	Asp	Pro	Val	Asn	Tyr	Ile	Leu	Gln	Val	Leu	Val
	370					375					380				
Gly	Arg	Glu	Ser	Glu	Tyr	Lys	Gln	Val	Tyr	Lys	Gly	Glu	Glu	Ala	Thr
385					390					395				400	
Phe	Gln	Ile	Ser	Gly	Leu	Gln	Thr	Asn	Thr	Asp	Tyr	Arg	Phe	Arg	Val
				405				410					415		
Cys	Ala	Cys	Arg	Arg	Cys	Leu	Asp	Thr	Ser	Gln	Glu	Leu	Ser	Gly	Ala

	420		425		430
Phe Ser Pro Ser Ala Ala Phe Val Leu Gln Arg Ser Glu Val Met Leu					
	435		440		445
Thr Gly Asp Met Gly Ser Leu Asp Asp Pro Lys Met Lys Ser Met Met					
	450		455		460
Pro Thr Asp Glu Gln Phe Ala Ala Ile Ile Val Leu Gly Phe Ala Thr					
465		470		475	480
Leu Ser Ile Leu Phe Ala Phe Ile Leu Gln Tyr Phe Leu Met Lys					
	485		490		495

<210> 61
 <211> 2384
 <212> DNA
 <213> Homo sapiens

<400> 61
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 atcgccctaa aggactggca ttcactgatg tggatgtcga ttccatcaaa attgcttggg 180
 aaagcccaca ggggcaagtt tccaggtaca ggggtgacct ctcgagccct gaggatggaa 240
 tccatgagct attccctgca cctgatgggtg aagaagacac tgcagagctg caaggcctca 300
 gaccgggttc tgagtacaca gtcagtgtgg ttgccttgca cgatgatatg gagagccagc 360
 ccctgattgg aacccagttc acagctattc ctgcaccaac tgacctgaag ttcactcagg 420
 tcacacccac aagcctgagc gccagtgga caccaccaa tgttcagctc actggatata 480
 gagtgcgggt gacccccaag gagaagaccg gaccaatgaa agaaatcaac cttgctcctg 540
 acagctcatc cgtggttgta tcaggactta tgggtggccac caaatatgaa gtgagtgtct 600
 atgctcttaa ggacactttg acaagcagac cagctcaggg tgttgtcacc actctggaga 660
 atgtcagccc accaagaagg gctcgtgtga cagatgttac tgagaccacc atcaccatta 720
 gctggagaac caagactgag acgatcactg gcttccaagt tgatgccgtt ccagccaatg 780
 gccagactcc aatccagaga accatcaagc cagatgtcag aagctacacc atcacaggtt 840
 tacaaccagg cactgactac aagatctacc tgtacacctt gaatgacaat gtcggagct 900
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<210> 62

<211> 793

<212> PRT

<213> Homo sapiens

<400> 62

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		20					25					30			
Gln	Thr	Ala	Val	Thr	Asn	Ile	Asp	Arg	Pro	Lys	Gly	Leu	Ala	Phe	Thr
	35					40					45				
Asp	Val	Asp	Val	Asp	Ser	Ile	Lys	Ile	Ala	Trp	Glu	Ser	Pro	Gln	Gly
50					55						60				
Gln	Val	Ser	Arg	Tyr	Arg	Val	Thr	Tyr	Ser	Ser	Pro	Glu	Asp	Gly	Ile
65				70					75					80	
His	Glu	Leu	Phe	Pro	Ala	Pro	Asp	Gly	Glu	Glu	Asp	Thr	Ala	Glu	Leu
			85						90					95	
Gln	Gly	Leu	Arg	Pro	Gly	Ser	Glu	Tyr	Thr	Val	Ser	Val	Val	Ala	Leu
		100					105					110			
His	Asp	Asp	Met	Glu	Ser	Gln	Pro	Leu	Ile	Gly	Thr	Gln	Ser	Thr	Ala
	115						120					125			
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser
130					135						140				
Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg
145				150					155					160	
Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn
			165						170					175	
Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala
		180					185					190			
Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser
	195						200					205			
Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro
	210					215					220				
Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser
225				230					235					240	
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val
			245						250					255	
Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val
		260					265					270			
Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile
	275					280						285			
Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile
	290				295						300				
Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	Ala
305				310					315					320	
Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro	Pro	Arg	Ala	Arg
			325						330					335	
Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg
	340							345					350		
Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr
	355						360					365			
Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys
	370					375					380				
Asn	Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu
385				390					395					400	
Leu	Pro	Gln	Leu	Val	Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu
			405					410					415		
Ile	Leu	Asp	Val	Pro	Ser	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val	Thr	His
		420						425					430		

Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly
 435 440 445
 Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe
 450 455 460
 Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro
 465 470 475 480
 Arg Pro Tyr Pro Pro Asn Val Gly Glu Glu Ile Gln Ile Gly His Ile
 485 490 495
 Pro Arg Glu Asp Val Asp Tyr His Leu Tyr Pro His Gly Pro Gly Leu
 500 505 510
 Asn Pro Asn Ala Ser Thr Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile
 515 520 525
 Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His
 530 535 540
 Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr
 545 550 555 560
 Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn
 565 570 575
 Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu
 580 585 590
 Glu Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro
 595 600 605
 Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val
 610 615 620
 Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys
 625 630 635 640
 Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg
 645 650 655
 Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp
 660 665 670
 Arg Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn
 675 680 685
 Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp
 690 695 700
 Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu
 705 710 715 720
 Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg
 725 730 735
 Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr
 740 745 750
 Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr
 755 760 765
 Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val
 770 775 780
 Gln Ala Asp Arg Glu Asp Ser Arg Glu
 785 790

<210> 63
 <211> 7680
 <212> DNA
 <213> Homo sapiens

<400> 63
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 gacctaccta ggtaattgtg tggttgttac ttgttatgga ggaagccgag gttttaactg 180
 cgaaagtaaa cctgaagctg aagagacttg ctttgacaag tacactggga acacttaccg 240
 agtgggtgac acttatgagc gtcctaaaga ctccatgatc tgggactgta cctgcatcgg 300

ggctgggcca	gggagaataa	gctgtacat	cgcaaaccgc	tgccatgaag	ggggtcagtc	360
ctacaagatt	ggtgacacct	ggaggagacc	acatgagact	ggtgggttaca	tgtagagtg	420
tgtgtgtctt	ggtaatggaa	aaggagaatg	gacctgcaag	cccatagctg	agaagtgttt	480
tgatcatgct	gctgggactt	cctatgtggt	cggagaaacg	tgggagaagc	cctaccaagg	540
ctggatgatg	gtagattgta	cttgccctggg	agaaggcagc	ggacgcatca	cttgcaacttc	600
tagaaataga	tgcaacgatc	aggacacaag	gacatcctat	agaattggag	acacctggag	660
caagaaggat	aatcgaggaa	acctgctcca	gtgcatctgc	acaggcaacg	gccgaggaga	720
gtggaagtgt	gagaggcaca	cctctgtgca	gaccacatcg	agcggatctg	gccccctcac	780
cgatgttcgt	gcagctgttt	accaaccgca	gcctcacccc	cagcctcctc	cctatggcca	840
ctgtgtcaca	gacagtgggtg	tggtctactc	tgtggggatg	cagtgggttga	agacacaagg	900
aaataatgcaa	atgctttgca	cgtgcctggg	cgacggagtc	agctgccaaag	agacagctgt	960
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<211> 2328

<212> PRT

<213> Homo sapiens

<400> 64

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<210> 69

<211> 756

<212> PRT

<213> Homo sapiens

<400> 69

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Lys	Gln	Asp	Pro	Ser	Asn	Ser	Lys	Asn	Ile	Ser	Lys	His	Gly	Gln	Asn
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Asn	Pro	Val	Gly	Asp	Tyr	Glu	His	Ala	Asp	Asp	Gln	Ala	Glu	Glu	Asp
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Ser	Gln	Asn	Lys	Asp	Lys	Thr	Leu	Glu	Lys	His	Leu	Lys	Thr	Val	Glu
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Leu	Asn	Ile	Ala	Leu	Ser	Gly	Lys	Phe	Gly	Asn	Ala	Val	Asn	Thr	Arg
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Ile	Leu	Lys	Cys	Met	Ile	Pro	Ala	Thr	Val	Ile	Ser	Glu	Asp	Ser	Val
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Val	Lys	Ala	Val	Ser	Trp	Leu	Cys	Val	Gly	Lys	Cys	Ser	Gly	Ser	Thr
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Lys	Val	Leu	Phe	Tyr	Arg	Trp	Leu	Val	Ala	Met	Phe	Asp	Phe	Ile	Asp
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Arg	Lys	Glu	Gln	Ile	Asn	Leu	Leu	Tyr	Gly	Phe	Phe	Phe	Ala	Ser	Leu
		180						185					190		
Gln	Asp	Asp	Ala	Leu	Cys	Pro	Tyr	Val	Cys	His	Leu	Leu	Tyr	Leu	Leu
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225				230						235					240
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Phe	Leu	Asp	Thr	Ile	Ile	Arg	Ala	Glu	Cys	Phe	Leu	Gln	Glu	Gly
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Leu	Lys	Glu	Leu	Leu	Gln	Asn	Trp	Leu	Leu	Trp	Leu	Ser	Met	Asp
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Phe	Ala	Lys	Gly	Ile	Tyr	Ile	Asp	Pro	Glu	Ile	Leu	Glu	Lys	Thr
			660				665						670	Gly
Val	Ala	Glu	Tyr	Lys	Asn	Ser	Leu	Asn	Val	Val	His	His	Pro	Ser
	675					680					685			Phe
Leu	Ser	Tyr	Ala	Val	Ser	Phe	Leu	Leu	Gln	Glu	Ser	Pro	Glu	Glu
	690					695				700				Arg
Thr	Val	Asn	Val	Ser	Ser	Ile	Arg	Gly	Lys	Lys	Trp	Ser	Trp	Tyr
705				710						715				Leu
Asp	Tyr	Leu	Phe	Ser	Gln	Gly	Leu	Gln	Gly	Leu	Lys	Leu	Phe	Ile
			725					730						Arg
Ser	Ser	Val	His	His	Ser	Ser	Ile	Pro	Arg	Ala	Glu	Gly	Ile	Asn
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 <212> DNA
 <213> Homo sapiens

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<210> 71

<211> 338

<212> PRT

<213> Homo sapiens

<400> 71

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Gly Val Asn Asp Ser Phe Pro Asp Gly Asp Tyr Asp Ala Asn Leu Glu
35          40          45
Ala Ala Ala Pro Cys His Ser Cys Asn Leu Leu Asp Asp Ser Ala Leu
50          55          60
Pro Phe Phe Ile Leu Thr Ser Val Leu Gly Ile Leu Ala Ser Ser Thr
65          70          75          80
Val Leu Phe Met Leu Phe Arg Pro Leu Phe Arg Trp Gln Leu Cys Pro
85          90          95
Gly Trp Pro Val Leu Ala Gln Leu Ala Val Gly Ser Ala Leu Phe Ser
100          105          110
Ile Val Val Pro Val Leu Ala Pro Gly Leu Gly Ser Thr Arg Ser Ser
115          120          125
Ala Leu Cys Ser Leu Gly Tyr Cys Val Trp Tyr Gly Ser Ala Phe Ala
130          135          140
Gln Ala Leu Leu Leu Gly Cys His Ala Ser Leu Gly His Arg Leu Gly
145          150          155          160
Ala Gly Gln Val Pro Gly Leu Thr Leu Gly Leu Thr Val Gly Ile Trp
165          170          175
Gly Val Ala Ala Leu Leu Thr Leu Pro Val Thr Leu Ala Ser Gly Ala
180          185          190
Ser Gly Gly Leu Cys Thr Leu Ile Tyr Ser Thr Glu Leu Lys Ala Leu
195          200          205
Gln Ala Thr His Thr Val Ala Cys Leu Ala Ile Phe Val Leu Leu Pro
210          215          220
Leu Gly Leu Phe Gly Ala Lys Gly Leu Lys Lys Ala Leu Gly Met Gly
225          230          235          240

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Pro Gly Pro Trp Met Asn Ile Leu Trp Ala Trp Phe Ile Phe Trp Trp
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 Pro His Gly Val Val Leu Gly Leu Asp Phe Leu Val Arg Ser Lys Leu
 260 265 270
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 275 280 285
 Asn Leu Ala Glu Ala Leu Ala Ile Leu His Cys Val Ala Thr Pro Leu
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<210> 72
 <211> 817
 <212> DNA
 <213> Homo sapiens

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<210> 73
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 73
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 20 25 30
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 35 40 45
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 50 55 60
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 65 70 75 80
 Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
 85 90 95
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Glu Glu
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<210> 74
<211> 2861
<212> DNA
<213> Homo sapiens

<400> 74

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 <212> PRT
 <213> Homo sapiens

<400> 75
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 35 40 45
 Arg Glu Ile Val Ala Leu Lys Thr Lys Leu Lys Glu Cys Glu Ala Ser
 50 55 60
 Lys Asp Gln Asn Thr Pro Val Val His Pro Pro Thr Pro Gly Ser
 65 70 75 80
 Cys Gly His Gly Gly Val Val Asn Ile Ser Lys Pro Ser Val Val Gln
 85 90 95
 Leu Asn Trp Arg Gly Phe Ser Tyr Leu Tyr Gly Ala Trp Gly Arg Asp
 100 105 110
 Tyr Ser Pro Gln His Pro Asn Lys Gly Leu Tyr Trp Val Ala Pro Leu
 115 120 125
 Asn Thr Asp Gly Arg Leu Leu Glu Tyr Tyr Ile Leu Tyr Asn Thr Leu
 130 135 140
 Asp Asp Leu Leu Leu Tyr Ile Asn Ala Arg Glu Leu Arg Ile Thr Tyr
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 180 185

<210> 76
 <211> 956
 <212> DNA
 <213> Homo sapiens

<400> 76
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 <212> PRT
 <213> Homo sapiens

<400> 77

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 Glu Asp Ala His Leu Thr Gln Tyr Lys Lys Glu Pro Val Thr Thr Arg
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<211> 1689

<212> DNA

<213> Homo sapiens

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 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 79

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 <213> Homo sapiens

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 <213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 2701

<212> PRT

<213> Homo sapiens

<400> 83

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35      40      45
Gly Ile Ser Arg Arg Met Pro Pro Ala Asn Leu Pro Ser Leu Lys
50      55      60
Ala Glu Asn Lys Gly Asn Asp Pro Asn Val Asn Ile Val Pro Lys Asp
65      70      75      80
Gly Thr Gly Trp Ala Ser Lys Gln Glu Gln His Glu Glu Glu Lys Thr
85      90      95
Pro Glu Val Pro Pro Ala Gln Pro Lys Pro Gly Val Ala Ala Pro Pro
100      105      110
Glu Val Ala Pro Ala Pro Lys Ser Trp Ala Ser Asn Lys Gln Gly Gly
115      120      125
Gln Gly Asp Gly Ile Gln Val Asn Ser Gln Phe Gln Gln Glu Phe Pro
130      135      140
Ser Leu Gln Ala Ala Gly Asp Gln Glu Lys Lys Glu Lys Glu Thr Asn
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210      215      220
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Glu Thr Asn Lys Gly Leu Arg Gly Arg Gly Pro Pro Pro Ser Trp Ala
275      280      285

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 Ala Gln Gln Gln Gln Asn Pro Gln Val Tyr Val Ser Gln Ser Ala Ala
 2370 2375 2380
 Ala Gln Ile Pro Ala Phe Tyr Met Asp Thr Ser His Leu Phe Asn Thr
 2385 2390 2395 2400
 Gln His Ala Arg Leu Ala Pro Pro Ser Leu Ala Gln Gln Gln Gly Phe
 2405 2410 2415
 Gln Pro Gly Leu Ser Gln Pro Thr Ser Val Gln Gln Ile Pro Ile Pro
 2420 2425 2430
 Ile Tyr Ala Pro Leu Gln Gly Gln His Gln Ala Gln Leu Ser Leu Gly
 2435 2440 2445
 Ala Gly Pro Ala Val Ser Gln Ala Gln Glu Leu Phe Ser Ser Ser Leu
 2450 2455 2460
 Gln Pro Tyr Arg Ser Gln Pro Ala Phe Met Gln Ser Ser Leu Ser Gln
 2465 2470 2475 2480
 Pro Ser Val Val Leu Ser Gly Thr Ala Ile His Asn Phe Pro Thr Val
 2485 2490 2495
 Gln His Gln Glu Leu Ala Lys Ala Gln Ser Gly Leu Ala Phe Gln Gln
 2500 2505 2510
 Thr Ser Asn Thr Gln Pro Ile Pro Ile Leu Tyr Glu His Gln Leu Gly
 2515 2520 2525
 Gln Ala Ser Gly Leu Gly Gly Ser Gln Leu Ile Asp Thr His Leu Leu
 2530 2535 2540
 Gln Ala Arg Ala Asn Leu Thr Gln Ala Ser Asn Leu Tyr Ser Gly Gln
 2545 2550 2555 2560
 Val Gln Gln Pro Gly Gln Thr Asn Phe Tyr Asn Thr Ala Gln Ser Pro
 2565 2570 2575
 Ser Ala Leu Gln Gln Val Thr Val Pro Leu Pro Ala Ser Gln Leu Ser
 2580 2585 2590
 Leu Pro Asn Phe Gly Ser Thr Gly Gln Pro Leu Ile Ala Leu Pro Gln
 2595 2600 2605
 Thr Leu Gln Pro Pro Leu Gln His Thr Thr Pro Gln Ala Gln Ala Gln
 2610 2615 2620
 Ser Leu Ser Arg Pro Ala Gln Val Ser Gln Pro Phe Arg Gly Leu Ile
 2625 2630 2635 2640
 Pro Ala Gly Thr Gln His Ser Met Ile Ala Thr Thr Gly Lys Met Ser

	2645		2650		2655
Glu Met	Glu Lys Ala Phe Gly	Ser Gly Ile Asp Ile	Lys Pro Gly		
	2660	2665	2670		
Thr Pro	Pro Ile Ala Gly Arg Ser	Thr Thr Pro Thr Ser	Ser Pro Ser		
	2675	2680	2685		
Gly Leu	Leu Leu Gln Val Arg Thr	Ala Ser Pro Ala Lys			
	2690	2695	2700		

<210> 84
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 84
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 ggctctgccc tagttttgcc cctggccagg attgctacag ttgtgattgg aggagttgtg 180
 gccatggcgg ctgtgcccat ggtgctcagt gccatgggct tcaactgcggc gggaatcgcc 240
 tcgtcctcca tagcagccaa gatgatgtcc gcggcgccca ttgccaatgg ggggtggagtt 300
 gcctcgggca gccttggtgg tactctgcag tcaactgggag caactggact ctccggattg 360
 accaagttca tcctgggctc cattgggtct gccattgcgg ctgtcattgc gaggttctac 420
 tagctccctg cccctcgccc tgcagagaag agaaccatgc cagggggagaa ggcacccagc 480
 catcctgacc cagcgaggag ccaactatcc caaatatacc tgggtgaaat ataccaaatt 540
 ctgcatctcc agaggaaaat aagaaataaa gatgaattgt tgcaactctt aaaaaaa 597

<210> 85
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 85
 Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
 1 5 10 15
 Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
 20 25 30
 Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Met Ala Ala Val Pro
 35 40 45
 Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser
 50 55 60
 Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly
 65 70 75 80
 Gly Val Ala Ser Gly Ser Leu Val Gly Thr Leu Gln Ser Leu Gly Ala
 85 90 95
 Thr Gly Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser
 100 105 110
 Ala Ile Ala Ala Val Ile Ala Arg Phe Tyr
 115 120

<210> 86
 <211> 1032
 <212> DNA
 <213> Homo sapiens

<400> 86
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 gctggacgtc cccacggcgg cggtgcaggc gtcccctctg caagcgtag acttcttttg 180

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gaatgggcca ccagttaact acaagacagg caatctatac ctgcgggggc ccctgaagaa 240
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aactagttta at 1032

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<210> 87

<211> 303

<212> PRT

<213> Homo sapiens

<400> 87

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Met Asp Ser Arg His Thr Phe Ala Pro Ala Ala Met Thr Leu Ser Pro
1          5          10          15
Leu Leu Leu Phe Leu Pro Pro Leu Leu Leu Leu Leu Asp Val Pro Thr
20          25          30
Ala Ala Val Gln Ala Ser Pro Leu Gln Ala Leu Asp Phe Phe Gly Asn
35          40          45
Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu Tyr Leu Arg Gly Pro
50          55          60
Leu Lys Lys Ser Asn Ala Pro Leu Val Asn Val Thr Leu Tyr Tyr Glu
65          70          75          80
Ala Leu Cys Gly Gly Cys Arg Ala Phe Leu Ile Arg Glu Leu Phe Pro
85          90          95
Thr Trp Leu Leu Val Met Glu Ile Leu Asn Val Thr Ser Val Pro Tyr
100          105          110
Gly Asn Ala Gln Glu Gln Asn Val Ser Gly Arg Trp Glu Phe Lys Cys
115          120          125
Gln Leu Gly Glu Glu Glu Cys Lys Phe Asn Lys Val Glu Ala Cys Val
130          135          140
Leu Asp Glu Leu Asp Met Glu Leu Ala Phe Leu Thr Met Ser Gly Met
145          150          155          160
Ala Trp Lys Ser Leu Arg Thr Trp Arg Glu Val Cys His Tyr Ala Cys
165          170          175
Ser Ser Thr Pro Gln Gly Cys Arg Gln Asn Tyr His Gly Val Cys Asn
180          185          190
Gly Gly Pro Arg His Ala Ala His Ala Arg Gln Arg Pro Ala Asp Arg
195          200          205
Cys Ser Pro Ala Thr Ala Arg Val Cys Ala Leu Gly His Arg Gln Trp
210          215          220
Glu Thr Leu Gly Arg Ser Asp Pro Ala Pro Tyr Pro Cys Leu Pro Val
225          230          235          240
Val Pro Gly Gln Glu Ala Gly Cys Leu Pro Phe Leu Asn Gln Leu Pro
245          250          255
Pro Glu Cys Leu Leu Arg Val Leu Ala Gly Gly Leu Arg Arg Ala His
260          265          270
Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe Ser Asp Pro Asp
275          280          285
Pro Arg His Leu Leu Leu Thr Asn Trp Lys Ile Leu Cys Ile Pro

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290

295

300

<210> 88
 <211> 905
 <212> DNA
 <213> Homo sapiens

<400> 88
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 taatttgatc ctcaggaatt tgttctgccc tcatctggcc ctggccagct ctgcatttga 180
 caaatgccag gaagaggaaa ctgttgagaa aacggaacta ctggggaaag ggagggctca 240
 ctgagaacca tcccggtaac ccgaccgccg ctggtcacca tgaaccacat tgtgcaaacc 300
 ttctctcctg tcaacagcgg ccagcctccc aactacgaga tgctcaagga ggagcaggaa 360
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 cgcagcgaga cctccgtgcc tgaccatgtc gtctggtccc tgttcaaac cctcttcctg 480
 aacacctgct gcctgggctt catagcattc gcctactcog tgaagtctag ggacaggaag 540
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 gtatcccacg tactctatct tccattcctc gccctgcccc cagaggccag gagctctgcc 780
 cttgacctgt attccactta ctccaccttc cattcctcgc cctgtcccca cagccgagtc 840
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 tttct 905

<210> 89
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 89
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 Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met Leu Gly
 20 25 30
 Gly Pro His Asn Pro Ala Pro Pro Thr Ser Thr Val Ile His Ile Arg
 35 40 45
 Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr
 50 55 60
 Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser
 65 70 75 80
 Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln
 85 90 95
 Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu
 100 105 110
 Gly Ile Phe Met Thr Ile Leu Leu Val Ile Ile Pro Val Leu Val Val
 115 120 125
 Gln Ala Gln Arg
 130

<210> 90
 <211> 2499
 <212> DNA
 <213> Homo sapiens

<400> 90
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<210> 91

<211> 291

<212> PRT

<213> Homo sapiens

<400> 91

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Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
 1             5             10             15
Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly
      20             25             30
Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
      35             40             45
Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
      50             55             60
Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
      65             70             75             80
Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro

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[illegible]

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<210> 92
<211> 1639
<212> DNA
<213> Homo sapiens
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<400>	92						
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ctgcagctct	gtgtgaaggt	gcagcttttg	caaggagtgc	taaagaactt	agatgtcagt	180	
gcataaagac	atactccaaa	cctttccacc	ccaaatttat	caaaagaactg	agatgtattg	240	
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aagtaaaaaa aaaaaaaaaa 1639

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<210> 93
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 93
 Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
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 20 25 30
 Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35 40 45
 Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
 50 55 60
 Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
 65 70 75 80
 Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
 85 90 95
 Glu Asn Ser

<210> 94
 <211> 1840
 <212> DNA
 <213> Homo sapiens

<400> 94
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 aagtgtctgg attatagtga ggagttcccc caccacagga tccgaggggc acagcgcggc 180
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 aatgaatgaa cttatggagc agacctcgga gatcatcacg tttgccgagt caggaacagc 480
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 aaaaaacaa aagtaaatta aaaacaaacc tgatgaaaca gatgaaacag atgaaggaag 1560


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atgtggaaat cttagcctgc cttagccagg gctcagagat gaagcagtga agagacagat 1620
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<210> 95

<211> 426

<212> PRT

<213> Homo sapiens

<400> 95

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Met Pro Leu Leu Trp Leu Arg Gly Phe Leu Leu Ala Ser Cys Trp Ile
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Ile Val Arg Ser Ser Pro Thr Pro Gly Ser Glu Gly His Ser Ala Ala
 20          25          30
Pro Asp Cys Pro Ser Cys Ala Leu Ala Leu Pro Lys Asp Val Pro
 35          40          45
Asn Ser Gln Pro Glu Met Val Glu Ala Val Lys Lys His Ile Leu Asn
 50          55          60
Met Leu His Leu Lys Lys Arg Pro Asp Val Thr Gln Pro Val Pro Lys
 65          70          75          80
Ala Ala Leu Leu Asn Ala Ile Arg Lys Leu His Val Gly Lys Val Gly
 85          90          95
Glu Asn Gly Tyr Val Glu Ile Glu Asp Asp Ile Gly Arg Arg Ala Glu
100          105          110
Met Asn Glu Leu Met Glu Gln Thr Ser Glu Ile Ile Thr Phe Ala Glu
115          120          125
Ser Gly Thr Ala Arg Lys Thr Leu His Phe Glu Ile Ser Lys Glu Gly
130          135          140
Ser Asp Leu Ser Val Val Glu Arg Ala Glu Val Trp Leu Phe Leu Lys
145          150          155          160
Val Pro Lys Ala Asn Arg Thr Arg Thr Lys Val Thr Ile Arg Leu Phe
165          170          175
Gln Gln Gln Lys His Pro Gln Gly Ser Leu Asp Thr Gly Glu Glu Ala
180          185          190
Glu Glu Val Gly Leu Lys Gly Glu Arg Ser Glu Leu Leu Leu Ser Glu
195          200          205
Lys Val Val Asp Ala Arg Lys Ser Thr Trp His Val Phe Pro Val Ser
210          215          220
Ser Ser Ile Gln Arg Leu Leu Asp Gln Gly Lys Ser Ser Leu Asp Val
225          230          235          240
Arg Ile Ala Cys Glu Gln Cys Gln Glu Ser Gly Ala Ser Leu Val Leu
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Asp Trp Ile Ile Ala Pro Ser Gly Tyr His Ala Asn Tyr Cys Glu Gly
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Gln Leu Ser Thr Ser	His Gln Asp Asn Leu Trp	Pro Met Ile Leu
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<210> 99

<211> 1066

<212> PRT

<213> Homo sapiens

<400> 99

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<213> Homo sapiens
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<211> 788

<212> PRT

<213> Homo sapiens

<400> 101

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Asp Cys Leu Leu Ile Gly Pro Gln Cys Ala Trp Cys Ala Gln Glu Asn
      35             40             45
Phe Thr His Pro Ser Gly Val Gly Glu Arg Cys Asp Thr Pro Ala Asn
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Leu Leu Ala Lys Gly Cys Gln Leu Asn Phe Ile Glu Asn Pro Val Ser
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Gln Val Glu Ile Leu Lys Asn Lys Pro Leu Ser Val Gly Arg Gln Lys
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Asn Ser Ser Asp Ile Val Gln Ile Ala Pro Gln Ser Leu Ile Leu Lys
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Leu Arg Pro Gly Gly Ala Gln Thr Leu Gln Val His Val Arg Gln Thr
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Glu Asp Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu Ser Ala Ser
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Met Asp Asp Asp Leu Asn Thr Ile Lys Glu Leu Gly Ser Arg Leu Ser
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Lys Glu Met Ser Lys Leu Thr Ser Asn Phe Arg Leu Gly Phe Gly Ser
      165            170            175
Phe Val Glu Lys Pro Val Ser Pro Phe Val Lys Thr Thr Pro Glu Glu
      180            185            190
Ile Ala Asn Pro Cys Ser Ser Ile Pro Tyr Phe Cys Leu Pro Thr Phe
      195            200            205
Gly Phe Lys His Ile Leu Pro Leu Thr Asn Asp Ala Glu Arg Phe Asn
      210            215            220
Glu Ile Val Lys Asn Gln Lys Ile Ser Ala Asn Ile Asp Thr Pro Glu
      225            230            235
Gly Gly Phe Asp Ala Ile Met Gln Ala Ala Val Cys Lys Glu Lys Ile
      245            250            255
Gly Trp Arg Asn Asp Ser Leu His Leu Leu Val Phe Val Ser Asp Ala
      260            265            270
Asp Ser His Phe Gly Met Asp Ser Lys Leu Ala Gly Ile Val Ile Pro
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Asn Asp Gly Leu Cys His Leu Asp Ser Lys Asn Glu Tyr Ser Met Ser
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Pro Pro Thr Ile His Tyr Pro Pro Ser Gln Gly Gln Met Asp Leu Cys
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      180      185      190
Phe Leu Tyr Thr Val Pro Asn Gly Asn Asn Pro Thr Gly Asn Ser Leu
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 <213> Homo sapiens

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<210> 105

<211> 408

<212> PRT

<213> Homo sapiens

<400> 105

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 Gly Ile Ser Leu Gln Glu Thr Thr Arg Ala Glu Thr Gly Met Ala Tyr
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 Arg Asn Leu Gly Lys Ser Gly Leu Arg Val Ser Cys Leu Gly Leu Gly
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 Tyr Trp Gly Gly Lys Ala Glu Thr Glu Arg Gly Leu Ser Arg Lys His
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 Glu Tyr His Leu Phe Gln Arg Glu Lys Val Glu Val Gln Leu Pro Glu
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<210> 106

<211> 3103

<212> DNA

<213> Homo sapiens

<400> 106

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<210> 107

<211> 419

<212> PRT

<213> Homo sapiens

<400> 107

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<210> 108

<211> 2620

<212> DNA

<213> Homo sapiens

<400> 108

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<210> 109

<211> 401

<212> PRT

<213> Homo sapiens

<400> 109

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Val Asn Ala Ala Arg Ala Lys Phe Arg Thr Val Ala Ile Ile Ala Arg
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 85 90 95
 Gln Ile Ser Asp Glu Val Ala Glu Arg Leu Met Thr Ile Ala Tyr Glu
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<210> 110
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 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens

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Val Pro Cys Asn Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser
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Arg Cys Gln Glu Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg
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Leu	Ser	Thr	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln		
				885					890					895			
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn		
		900						905					910				
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn		
		915					920					925					
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr		
	930					935					940						
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu		
945					950					955					960		
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu		
			965						970					975			
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln		
			980					985					990				
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys		
		995					1000					1005					
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu		
	1010					1015					1020						
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu		
1025					1030					1035					1040		

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val
 1045 1050 1055
 Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp
 1060 1065 1070
 Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala
 1075 1080 1085
 Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly
 1090 1095 1100
 Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu
 1105 1110 1115 1120
 Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser
 1125 1130 1135
 Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln
 1140 1145 1150
 Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala
 1155 1160 1165
 Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys
 1170 1175 1180
 Tyr Asn Thr Gln Ala Leu Glu Gln Gln
 1185 1190

<210> 116
 <211> 749
 <212> DNA
 <213> Homo sapiens

<400> 116
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 ctaggatttg atgactttgt caatatggta ctggaagatg tcaactgagtt tgaaatcaca 180
 ccagaaggaa gaaggattac taaattagat cagattttgc taaatggaaa taatataaca 240
 atgctgggttc ctggaggaga aggacctgaa gtgtgaatga gtttccttga cttacactag 300
 attttgtttt ggcttataat gacaagaaaa tggaaattttt tttcccaactt tctaattgtt 360
 aaatcccata aagctaagtt tcccgttaaa ggaagtgct ttgaagatgt gtaccattt 420
 ttgtaagtta atcatgatta tcctggaaaa agaagaaaaa aacttcttct tttgcagatg 480
 aaaataaagg tgttttttgt taactgtcat tttgtttatt ctactgcagt agccagtgga 540
 acaaagtttg tagttatttt gccacttact tttctgtcat tatatgctta tttgttttgt 600
 catttacgtg accatttgat tctcaaacaa aagttgttcc aaacaaaatg atgaactttg 660
 atttgaacag gtgcatttaa acaaccggaa atgatcactt agaaaattca attaaaatgc 720
 tgttgttttg taaaaaaaaa aaaaaaaaaa 749

<210> 117
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 117
 Met Ala Ala Asn Ala Thr Thr Asn Pro Ser Gln Leu Leu Pro Leu Glu
 1 5 10 15
 Leu Val Asp Lys Cys Ile Gly Ser Arg Ile His Ile Val Met Lys Ser
 20 25 30
 Asp Lys Glu Ile Val Gly Thr Leu Leu Gly Phe Asp Asp Phe Val Asn
 35 40 45
 Met Val Leu Glu Asp Val Thr Glu Phe Glu Ile Thr Pro Glu Gly Arg
 50 55 60
 Arg Ile Thr Lys Leu Asp Gln Ile Leu Leu Asn Gly Asn Asn Ile Thr
 65 70 75 80
 Met Leu Val Pro Gly Gly Glu Gly Pro Glu Val

85

90

<210> 118
 <211> 1717
 <212> DNA
 <213> Homo sapiens

<400> 118
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 attgggtggtta ccagtggtcca gtactatgat tatgatcttc ccctatcaat ttatgggcaa 180
 tcatcaccaa actgtgcacc agaattgtaac tgccctgaaa gctacccaag tgccatgtac 240
 tgtgatgagc tgaaattgaa aagtgtacca atgggtgcctc ctggaatcaa gtatctttac 300
 cttaggaata accagattga ccatattgat gaaaaggcct ttgagaatgt aactgatctg 360
 cagtggtctca ttctagatca caaccttcta gaaaactcca agataaaaagg gagagttttc 420
 tctaaattga aacaactgaa gaagctgcat ataaaccaca acaacctgac agagtctgtg 480
 ggcccacttc ccaaactctc ggaggatctg cagcttactc ataacaagat cacaagctg 540
 ggctcttttg aaggattggt aaacctgacc ttcatccatc tccagcacia tgggtgaaa 600
 gaggatgctg tttcagctgc ttttaaaggc cttaaatcac tccaatacct tgacttgagc 660
 ttcaatcaga tagccagact gccttctggt ctccctgtct ctcttctaac tctctactta 720
 gacaacaata agatcagcaa catccctgat gagtatttca agcgtttttaa tgcattgcag 780
 tatctgcgtt tatctcacia cgaactggct gatagtggaa tacctggaaa ttctttcaat 840
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 aacgaagtca ctcttaatta atatctgtat cctggaacaa tattttatgg ttatgttttt 1140
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 aaaatctgag ggaaatgttt tgtaaacatt tatttttttt aaagaaaaga tgaaaggcag 1260
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 tggtaaaaaa atagggtgga gatattgagg ccaagaatat tgcaaaatat atgaagcttc 1560
 atgcacttaa agaagtattt ttagaataag aatttgcata cttacctagt gaaacttttc 1620
 tagaattatt tttcactcta agtcatgtat gtttctcttt gattattttgc atgttatgtt 1680
 taataagcta ctagcaaaat aaaacatagc aaatggc 1717

<210> 119
 <211> 338
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
 1 5 10 15
 Ser Gly Gln Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln
 20 25 30
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 35 40 45
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val
 50 55 60
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Gln Ile Asp His
 65 70 75 80
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile
 85 90 95
 Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe
 100 105 110

Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu
 115 120 125
 Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu
 130 135 140
 Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn
 145 150 155 160
 Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val
 165 170 175
 Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser
 180 185 190
 Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu
 195 200 205
 Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr
 210 215 220
 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu
 225 230 235 240
 Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu
 245 250 255
 Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val
 260 265 270
 Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys
 275 280 285
 Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser
 290 295 300
 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser
 305 310 315 320
 Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr
 325 330 335
 Leu Asn

<210> 120

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 120

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 caatggagac ttatcccccagggtgaagg ggagtcgccc cctgtgaacg gaacagatga 180
 ggcagccggg gccactggcg atgccatcga gccagcacc cctagccagg gtgctgaggc 240
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 gcctttcaaa ttgagcggcc tgtccttcaa gagaaatcgg aaggagggtg ggggtgattc 360
 ttctgcctcc tcaccacacag aggaagagca ggagcagggg gagatcgggt cctgcagcga 420
 cgagggcact gctcaggaag ggaaggccgc agccaccctc gagagccagg aaccccaggc 480
 caagggggca gaggctagtg cagcctcaga agaagaggca gggcccagg ctacagagcc 540
 atccactccc tcggggccgg agagtggccc tacaccagcc agcgctgagc agaatgagta 600
 gctaggtagg ggcaggtggg tgatctctaa gctgcaaaaa ctgtgctgtc cttgtgaggt 660
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 tgaacaact tcttgtcttt ttttctccca ctgttgtaaa taacttttaa tggccaaacc 1260

ccagatttgt actttttttt tttttctaac tgctaaaacc attctcttcc acctggtttt 1320
actgtaacat ttgg 1334

<210> 121
<211> 195
<212> PRT
<213> Homo sapiens

<400> 121
Met Gly Ser Gln Ser Ser Lys Ala Pro Arg Gly Asp Val Thr Ala Glu
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Glu Ala Ala Gly Ala Ser Pro Ala Lys Ala Asn Gly Gln Glu Asn Gly
20 25 30
His Val Lys Ser Asn Gly Asp Leu Ser Pro Lys Gly Glu Gly Glu Ser
35 40 45
Pro Pro Val Asn Gly Thr Asp Glu Ala Ala Gly Ala Thr Gly Asp Ala
50 55 60
Ile Glu Pro Ala Pro Pro Ser Gln Gly Ala Glu Ala Lys Gly Glu Val
65 70 75 80
Pro Pro Lys Glu Thr Pro Lys Lys Lys Lys Lys Phe Ser Phe Lys Lys
85 90 95
Pro Phe Lys Leu Ser Gly Leu Ser Phe Lys Arg Asn Arg Lys Glu Gly
100 105 110
Gly Gly Asp Ser Ser Ala Ser Ser Pro Thr Glu Glu Glu Gln Glu Gln
115 120 125
Gly Glu Ile Gly Ala Cys Ser Asp Glu Gly Thr Ala Gln Glu Gly Lys
130 135 140
Ala Ala Ala Thr Pro Glu Ser Gln Glu Pro Gln Ala Lys Gly Ala Glu
145 150 155 160
Ala Ser Ala Ala Ser Glu Glu Glu Ala Gly Pro Gln Ala Thr Glu Pro
165 170 175
Ser Thr Pro Ser Gly Pro Glu Ser Gly Pro Thr Pro Ala Ser Ala Glu
180 185 190
Gln Asn Glu
195

<210> 122
<211> 1081
<212> DNA
<213> Homo sapiens

<400> 122
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gctgcctacc tcttctgct attcctgcct gcaggcttgc tggtcaggg ccagtatgat 180
ctggaccgcg tgccgccgtt ccctgaccac gtccagtaca cccactatag cgaccagatc 240
gacaaccag actactatga ttatcaagag gtgactctc ggccctccga ggaacagttc 300
cagttccagt cccagcagca agtccaacag gaagtcaccc cagccccaac ccagaacca 360
ggaaatgcag agctggagcc cacagagcct gggcctcttg actgccgtga ggaacagtac 420
ccgtgcaccc gcctctactc catacacagg ccttgcaaac agtgtctcaa cgaggtctgc 480
ttctacagcc tccgccgtgt gtacgtcatt aacaaggaga tctgtgttcg tacagtgtgt 540
gcccacgagg agctcctccg agctgacctc tgtcgggaca agttctccaa atgtggcgtg 600
atggccagca gcggcctgtg ccaatccgtg gcggcctcct gtgccaggag ctgtgggagc 660
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cccaggcctc tctgtgggac ctgggcctga cgggcccctc tcagcccgtt ttgaggacag 960

acagtcccc gaggtaggct acatcccccc accccagctg gtctgcttgg atttcctaca 1020
 gccccgtgg gcatggacca cctttatttt atacaaaatt aaaaacaagt ttttacaaaa 1080
 a 1081

<210> 123
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu
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 Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His
 20 25 30
 Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr
 35 40 45
 Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe
 50 55 60
 Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro
 65 70 75 80
 Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp
 85 90 95
 Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg
 100 105 110
 Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg
 115 120 125
 Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His
 130 135 140
 Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys
 145 150 155 160
 Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys
 165 170 175
 Ala Arg Ser Cys Gly Ser Cys
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<210> 124
 <211> 1066
 <212> DNA
 <213> Homo sapiens

<400> 124
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 ctgctattcc tgctgcagg cttgctggct cagggccagt atgatctgga cccgtgccc 180
 ccgttccttg accacgtcca gtacacccac tatagcgacc agatcgacaa ccagactac 240
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 tactccatac acaggccttg caaacagtgt ctcaacgagg tctgcttcta cagcctccgc 480
 cgtgtgtacg tcattaacaa ggagatctgt gttcgtacag tgtgtgccc cgaggagctc 540
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 gggacctggg cctgacgggc ccttctcagc ccgttttgag gacagacagt ccccgaggt 960
 aggctacatc cccccacccc agctgggtctg cttggatttc ctacagcccc cgtgggcatg 1020

gaccaccttt attttataca aaatttaaaaa caagttttta caaaaa

1066

<210> 125

<211> 183

<212> PRT

<213> Homo sapiens

<400> 125

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Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu
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          20           25           30
Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr
          35           40           45
Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe
 50           55           60
Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro
 65           70           75           80
Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp
          85           90           95
Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg
          100          105          110
Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg
          115          120          125
Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His
          130          135          140
Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys
145          150          155          160
Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys
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Ala Arg Ser Cys Gly Ser Cys
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<210> 126

<211> 1611

<212> DNA

<213> Homo sapiens

<400> 126

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cattatcttg accagctgaa tcacattttg ggtattcttg gatccccatc acaagaagac 1080
ctgaattgta taataaattt aaaagctagg aactatttgc tttctcttcc acacaaaaat 1140

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<210> 127
<211> 360
<212> PRT
<213> Homo sapiens
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<400>	127														
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Gln	Val	Phe	Asp	Val	Gly	Pro	Arg	Tyr	Thr	Asn	Leu	Ser	Tyr	Ile	Gly
			20					25					30		
Glu	Gly	Ala	Tyr	Gly	Met	Val	Cys	Ser	Ala	Tyr	Asp	Asn	Val	Asn	Lys
			35				40					45			
Val	Arg	Val	Ala	Ile	Lys	Lys	Ile	Ser	Pro	Phe	Glu	His	Gln	Thr	Tyr
	50					55					60				
Cys	Gln	Arg	Thr	Leu	Arg	Glu	Ile	Lys	Ile	Leu	Leu	Arg	Phe	Arg	His
65				70					75					80	
Glu	Asn	Ile	Ile	Gly	Ile	Asn	Asp	Ile	Ile	Arg	Ala	Pro	Thr	Ile	Glu
				85					90					95	
Gln	Met	Lys	Asp	Val	Tyr	Ile	Val	Gln	Asp	Leu	Met	Glu	Thr	Asp	Leu
			100					105					110		
Tyr	Lys	Leu	Leu	Lys	Thr	Gln	His	Leu	Ser	Asn	Asp	His	Ile	Cys	Tyr
			115				120					125			
Phe	Leu	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asn
	130					135					140				
Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Leu	Leu	Asn	Thr	Thr
145				150						155					160
Cys	Asp	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Val	Ala	Asp	Pro
				165					170					175	
Asp	His	Asp	His	Thr	Gly	Phe	Leu	Thr	Glu	Tyr	Val	Ala	Thr	Arg	Trp
			180					185					190		
Tyr	Arg	Ala	Pro	Glu	Ile	Met	Leu	Asn	Ser	Lys	Gly	Tyr	Thr	Lys	Ser
			195			200						205			
Ile	Asp	Ile	Trp	Ser	Val	Gly	Cys	Ile	Leu	Ala	Glu	Met	Leu	Ser	Asn
	210					215					220				
Arg	Pro	Ile	Phe	Pro	Gly	Lys	His	Tyr	Leu	Asp	Gln	Leu	Asn	His	Ile
225					230					235					240
Leu	Gly	Ile	Leu	Gly	Ser	Pro	Ser	Gln	Glu	Asp	Leu	Asn	Cys	Ile	Ile
				245					250					255	
Asn	Leu	Lys	Ala	Arg	Asn	Tyr	Leu	Leu	Ser	Leu	Pro	His	Lys	Asn	Lys
			260					265					270		
Val	Pro	Trp	Asn	Arg	Leu	Phe	Pro	Asn	Ala	Asp	Ser	Lys	Ala	Leu	Asp
			275			280						285			
Leu	Leu	Asp	Lys	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Glu	Val
	290					295					300				
Glu	Gln	Ala	Leu	Ala	His	Pro	Tyr	Leu	Glu	Gln	Tyr	Tyr	Asp	Pro	Ser
305					310					315					320
Asp	Glu	Pro	Ile	Ala	Glu	Ala	Pro	Phe	Lys	Phe	Asp	Met	Glu	Leu	Asp
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<210> 128
<211> 2917
<212> DNA
<213> Homo sapiens

<400> 128
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<210> 129
 <211> 821
 <212> PRT
 <213> Homo sapiens

<400> 129

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			20					25					30		
Phe	Leu	Glu	Glu	Phe	Gln	Ser	Ser	Asp	Gly	Glu	Ile	Lys	Tyr	Leu	Gln
		35					40					45			
Leu	Ala	Glu	Glu	Leu	Ile	Arg	Pro	Glu	Arg	Asn	Thr	Leu	Val	Val	Ser
	50					55					60				
Phe	Val	Asp	Leu	Glu	Gln	Phe	Asn	Gln	Gln	Leu	Ser	Thr	Thr	Ile	Gln
65					70				75						80
Glu	Glu	Phe	Tyr	Arg	Val	Tyr	Pro	Tyr	Leu	Cys	Arg	Ala	Leu	Lys	Thr
				85				90						95	
Phe	Val	Lys	Asp	Arg	Lys	Glu	Ile	Pro	Leu	Ala	Lys	Asp	Phe	Tyr	Val
			100					105					110		
Ala	Phe	Gln	Asp	Leu	Pro	Thr	Arg	His	Lys	Ile	Arg	Glu	Leu	Thr	Ser
		115					120					125			
Ser	Arg	Ile	Gly	Leu	Leu	Thr	Arg	Ile	Ser	Gly	Gln	Val	Val	Arg	Thr
	130					135					140				
His	Pro	Val	His	Pro	Glu	Leu	Val	Ser	Gly	Thr	Phe	Leu	Cys	Leu	Asp
145					150					155					160
Cys	Gln	Thr	Val	Ile	Arg	Asp	Val	Glu	Gln	Gln	Phe	Lys	Tyr	Thr	Gln
				165					170					175	
Pro	Asn	Ile	Cys	Arg	Asn	Pro	Val	Cys	Ala	Asn	Arg	Arg	Arg	Phe	Leu
			180					185					190		
Leu	Asp	Thr	Asn	Lys	Ser	Arg	Phe	Val	Asp	Phe	Gln	Lys	Val	Arg	Ile
		195					200					205			
Gln	Glu	Thr	Gln	Ala	Glu	Leu	Pro	Arg	Gly	Ser	Ile	Pro	Arg	Ser	Leu
	210					215						220			
Glu	Val	Ile	Leu	Arg	Ala	Glu	Ala	Val	Glu	Ser	Ala	Gln	Ala	Gly	Asp
225					230					235					240
Lys	Cys	Asp	Phe	Thr	Gly	Thr	Leu	Ile	Val	Val	Pro	Asp	Val	Ser	Lys
				245					250					255	
Leu	Ser	Thr	Pro	Gly	Ala	Arg	Ala	Glu	Thr	Asn	Ser	Arg	Val	Ser	Gly
			260					265					270		
Val	Asp	Gly	Tyr	Glu	Thr	Glu	Gly	Ile	Arg	Gly	Leu	Arg	Ala	Leu	Gly
		275					280					285			
Val	Arg	Asp	Leu	Ser	Tyr	Arg	Leu	Val	Phe	Leu	Ala	Cys	Cys	Val	Ala
		290					295				300				
Pro	Thr	Asn	Pro	Arg	Phe	Gly	Gly	Lys	Glu	Leu	Arg	Asp	Glu	Glu	Gln
305					310					315					320
Thr	Ala	Glu	Ser	Ile	Lys	Asn	Gln	Met	Thr	Val	Lys	Glu	Trp	Glu	Lys
				325					330					335	
Val	Phe	Glu	Met	Ser	Gln	Asp	Lys	Asn	Leu	Tyr	His	Asn	Leu	Cys	Thr
			340					345					350		
Ser	Leu	Phe	Pro	Thr	Ile	His	Gly	Asn	Asp	Glu	Val	Lys	Arg	Gly	Val
		355					360					365			
Leu	Leu	Met	Leu	Phe	Gly	Gly	Val	Pro	Lys	Thr	Thr	Gly	Glu	Gly	Thr
	370					375					380				
Ser	Leu	Arg	Gly	Asp	Ile	Asn	Val	Cys	Ile	Val	Gly	Asp	Pro	Ser	Thr
385					390					395					400
Ala	Lys	Ser	Gln	Phe	Leu	Lys	His	Val	Glu	Glu	Phe	Ser	Pro	Arg	Ala
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Val Tyr Thr Ser Gly Lys Ala Ser Ser Ala Ala Gly Leu Thr Ala Ala
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Val Val Arg Asp Glu Glu Ser His Glu Phe Val Ile Glu Ala Gly Ala
      435      440      445
Leu Met Leu Ala Asp Asn Gly Val Cys Cys Ile Asp Glu Phe Asp Lys
      450      455      460
Met Asp Val Arg Asp Gln Val Ala Ile His Glu Ala Met Glu Gln Gln
      465      470      475      480
Thr Ile Ser Ile Thr Lys Ala Gly Val Lys Ala Thr Leu Asn Ala Arg
      485      490      495
Thr Ser Ile Leu Ala Ala Ala Asn Pro Ile Ser Gly His Tyr Asp Arg
      500      505      510
Ser Lys Ser Leu Lys Gln Asn Ile Asn Leu Ser Ala Pro Ile Met Ser
      515      520      525
Arg Phe Asp Leu Phe Phe Ile Leu Val Asp Glu Cys Asn Glu Val Thr
      530      535      540
Asp Tyr Ala Ile Ala Arg Arg Ile Val Asp Leu His Ser Arg Ile Glu
      545      550      555      560
Glu Ser Ile Asp Arg Val Tyr Ser Leu Asp Asp Ile Arg Arg Tyr Leu
      565      570      575
Leu Phe Ala Arg Gln Phe Lys Pro Lys Ile Ser Lys Glu Ser Glu Asp
      580      585      590
Phe Ile Val Glu Gln Tyr Lys His Leu Arg Gln Arg Asp Gly Ser Gly
      595      600      605
Val Thr Lys Ser Ser Trp Arg Ile Thr Val Arg Gln Leu Glu Ser Met
      610      615      620
Ile Arg Leu Ser Glu Ala Met Ala Arg Met His Cys Cys Asp Glu Val
      625      630      635      640
Gln Pro Lys His Val Lys Glu Ala Phe Arg Leu Leu Asn Lys Ser Ile
      645      650      655
Ile Arg Val Glu Thr Pro Asp Val Asn Leu Asp Gln Glu Glu Glu Ile
      660      665      670
Gln Met Glu Val Asp Glu Gly Ala Gly Gly Ile Asn Gly His Ala Asp
      675      680      685
Ser Pro Ala Pro Val Asn Gly Ile Asn Gly Tyr Asn Glu Asp Ile Asn
      690      695      700
Gln Glu Ser Ala Pro Lys Ala Ser Leu Arg Leu Gly Phe Ser Glu Tyr
      705      710      715      720
Cys Arg Ile Ser Asn Leu Ile Val Leu His Leu Arg Lys Val Glu Glu
      725      730      735
Glu Glu Asp Glu Ser Ala Leu Lys Arg Ser Glu Leu Val Asn Trp Tyr
      740      745      750
Leu Lys Glu Ile Glu Ser Glu Ile Asp Ser Glu Glu Glu Leu Ile Asn
      755      760      765
Lys Lys Arg Ile Ile Glu Lys Val Ile His Arg Leu Thr His Tyr Asp
      770      775      780
His Val Leu Ile Glu Leu Thr Gln Ala Gly Leu Lys Gly Ser Thr Glu
      785      790      795      800
Gly Ser Glu Ser Tyr Glu Glu Asp Pro Tyr Leu Val Val Asn Pro Asn
      805      810      815
Tyr Leu Leu Glu Asp
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<210> 130

<211> 786

<212> DNA

<213> Homo sapiens

<400> 130

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cccggggagc gagtgcgctg agtgggctg gggggccctgc acccccagca gcaaggattg 180
cggcgtgggt ttccgcgagg gcacctgcgg ggcccagacc cagcgcatcc ggtgcagggt 240
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786

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<210> 131

<211> 143

<212> PRT

<213> Homo sapiens

<400> 131

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20          25          30
Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
35          40          45
Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
50          55          60
Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
65          70          75          80
Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
85          90          95
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
100         105         110
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
115         120         125
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
130         135         140

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<210> 132

<211> 603

<212> DNA

<213> Homo sapiens

<400> 132

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catggaatct tatgaactta atcccttcac taacaggaga aatgcaaata ccttcataatc 180
ccctcagcag agatggagag ctaaaagtcca agagaggatc cgagaacgct ctaagcctgt 240
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ctt
603

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<210> 133
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 133
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 20 25 30
 Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln
 35 40 45
 Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro
 50 55 60
 Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu
 65 70 75 80
 Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe
 85 90 95
 Arg Lys Arg Arg Gly Ala Lys
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<210> 134
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 134
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<210> 135
 <211> 470
 <212> PRT
 <213> Homo sapiens

<400> 135

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			20					25					30		
Gly	Glu	Arg	Tyr	Leu	Glu	Lys	Phe	Tyr	Gly	Leu	Glu	Ile	Asn	Lys	Leu
		35					40					45			
Pro	Val	Thr	Lys	Met	Lys	Tyr	Ser	Gly	Asn	Leu	Met	Lys	Glu	Lys	Ile
	50				55						60				
Gln	Glu	Met	Gln	His	Phe	Leu	Gly	Leu	Lys	Val	Thr	Gly	Gln	Leu	Asp
65				70						75				80	
Thr	Ser	Thr	Leu	Glu	Met	Met	His	Ala	Pro	Arg	Cys	Gly	Val	Pro	Asp
			85					90						95	
Leu	His	His	Phe	Arg	Glu	Met	Pro	Gly	Gly	Pro	Val	Trp	Arg	Lys	His
			100					105					110		
Tyr	Ile	Thr	Tyr	Arg	Ile	Asn	Asn	Tyr	Thr	Pro	Asp	Met	Asn	Arg	Glu
		115				120						125			
Asp	Val	Asp	Tyr	Ala	Ile	Arg	Lys	Ala	Phe	Gln	Val	Trp	Ser	Asn	Val
	130					135					140				
Thr	Pro	Leu	Lys	Phe	Ser	Lys	Ile	Asn	Thr	Gly	Met	Ala	Asp	Ile	Leu
145					150					155					160
Val	Val	Phe	Ala	Arg	Gly	Ala	His	Gly	Asp	Phe	His	Ala	Phe	Asp	Gly
			165					170						175	
Lys	Gly	Gly	Ile	Leu	Ala	His	Ala	Phe	Gly	Pro	Gly	Ser	Gly	Ile	Gly
			180					185					190		
Gly	Asp	Ala	His	Phe	Asp	Glu	Asp	Glu	Phe	Trp	Thr	Thr	His	Ser	Gly
	195					200						205			
Gly	Thr	Asn	Leu	Phe	Leu	Thr	Ala	Val	His	Glu	Ile	Gly	His	Ser	Leu
	210					215					220				
Gly	Leu	Gly	His	Ser	Ser	Asp	Pro	Lys	Ala	Val	Met	Phe	Pro	Thr	Tyr
225				230						235					240
Lys	Tyr	Val	Asp	Ile	Asn	Thr	Phe	Arg	Leu	Ser	Ala	Asp	Asp	Ile	Arg
			245						250					255	
Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Asp	Pro	Lys	Glu	Asn	Gln	Arg	Leu	Pro
		260						265					270		
Asn	Pro	Asp	Asn	Ser	Glu	Pro	Ala	Leu	Cys	Asp	Pro	Asn	Leu	Ser	Phe
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Asp	Ala	Val	Thr	Thr	Val	Gly	Asn	Lys	Ile	Phe	Phe	Phe	Lys	Asp	Arg
	290					295						300			
Phe	Phe	Trp	Leu	Lys	Val	Ser	Glu	Arg	Pro	Lys	Thr	Ser	Val	Asn	Leu
305					310					315					320
Ile	Ser	Ser	Leu	Trp	Pro	Thr	Leu	Pro	Ser	Gly	Ile	Glu	Ala	Ala	Tyr
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Glu	Ile	Glu	Ala	Arg	Asn	Gln	Val	Phe	Leu	Phe	Lys	Asp	Asp	Lys	Tyr
		340						345					350		
Trp	Leu	Ile	Ser	Asn	Leu	Arg	Pro	Glu	Pro	Asn	Tyr	Pro	Lys	Ser	Ile
	355					360						365			
His	Ser	Phe	Gly	Phe	Pro	Asn	Phe	Val	Lys	Lys	Ile	Asp	Ala	Ala	Val
	370					375					380				
Phe	Asn	Pro	Arg	Phe	Tyr	Arg	Thr	Tyr	Phe	Phe	Val	Asp	Asn	Gln	Tyr
385				390						395					400
Trp	Arg	Tyr	Asp	Glu	Arg	Arg	Gln	Met	Met	Asp	Pro	Gly	Tyr	Pro	Lys
			405						410					415	

Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile Asp Ala Val
 420 425 430
 Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly Ser Asn Gln
 435 440 445
 Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr Leu Lys Ser
 450 455 460
 Asn Ser Trp Phe Gly Cys
 465 470

<210> 136
 <211> 1821
 <212> DNA
 <213> Homo sapiens

<400> 136
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 aactactacg acctcaaaaa agatgtgaaa cagtttggtta ggagaaagga cagtggtcct 240
 gttgttaaaa aaatccgaga aatgcagaag ttccttggat tggaggtgac ggggaagctg 300
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<210> 137
 <211> 477
 <212> PRT
 <213> Homo sapiens

<400> 137
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<210> 138
<211> 1127

<212> DNA

<213> Homo sapiens

<400> 138

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<210> 139

<211> 267

<212> PRT

<213> Homo sapiens

<400> 139

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20      25      30
Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
35      40      45
Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
50      55      60
Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
65      70      75      80
Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
85      90      95
Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
100     105     110
Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
115     120     125
Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
130     135     140
Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
145     150     155     160
Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
165     170     175
Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
180     185     190
Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
195     200     205
Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
210     215     220
Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp

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225		230		235		240									
Pro	Gln	Asn	Phe	Lys	Leu	Ser	Gln	Asp	Asp	Ile	Lys	Gly	Ile	Gln	Lys
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Leu	Tyr	Gly	Lys	Arg	Ser	Asn	Ser	Arg	Lys	Lys					
			260					265							

<210> 140
 <211> 1078
 <212> DNA
 <213> Homo sapiens

<400> 140

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gccaacagtt	tagaagccaa	actcaaggag	atgcaaaaat	tctttggcct	acctataact	240
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<210> 141
 <211> 2334
 <212> DNA
 <213> Homo sapiens

<400> 141

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ccagaagcaa	ctgtccctgc	ccgagaccgg	tgagctggat	agcgccacgc	tgaaggccat	300
gcgaacccca	cggtgcgggg	tcccagacct	gggcagattc	caaacctttg	agggcgacct	360
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<210> 142

<211> 707

<212> PRT

<213> Homo sapiens

<400> 142

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 20          25          30
Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
 35          40          45
Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
 50          55          60
Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
 65          70          75          80
Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
 85          90          95
Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100          105          110
Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115          120          125
Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
130          135          140
Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145          150          155          160
Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165          170          175
Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180          185          190
Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195          200          205
Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210          215          220
Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225          230          235          240
Tyr Ser Ala Cys Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245          250          255
Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260          265          270

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Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys
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 290 295 300
 Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr
 305 310 315 320
 Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr
 325 330 335
 Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr
 340 345 350
 Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp
 355 360 365
 Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys
 370 375 380
 Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala
 385 390 395 400
 His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu
 405 410 415
 Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His
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 Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu
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 Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro
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 Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg
 465 470 475 480
 Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro
 485 490 495
 Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val
 500 505 510
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 515 520 525
 Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu
 530 535 540
 Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp
 545 550 555 560
 Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser
 565 570 575
 Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly
 580 585 590
 Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala
 595 600 605
 Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met
 610 615 620
 Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln
 625 630 635 640
 Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly
 645 650 655
 Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr
 660 665 670
 Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu
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<211> 2217
 <212> DNA
 <213> Homo sapiens

<400> 143
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<210> 144
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 144
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 Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
 35 40 45
 Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
 50 55 60
 Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
 65 70 75 80

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Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
		100						105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
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Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
	145				150					155					160
Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu
				165				170						175	
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
		180					185						190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
	195					200						205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215				220					
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
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Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245				250						255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
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Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
	275					280						285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
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Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
				325				330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
				340				345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355					360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375						380			
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
	385				390				395						400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
				405				410						415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
		420					425						430		
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		435					440					445			
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
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Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
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Glu	Glu	Arg	His	Arg	Pro	Val	Arg	Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln
			565						570					575	
Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn
			580						585					590	
Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser	Val	Gln	Gly	Gly	Arg	Gly	Gly	Gln
			595					600					605		
Ala	Arg	Ala	Gly	Gly	Arg	Ala	Gly	Gly	Val	Glu	Val	Gly	Ala	Leu	Ser
			610				615					620			
His	Pro	Ser	Leu	Cys	Arg	Gly	Pro	Leu	Gly	Asp	Ala	Leu	Pro	Pro	Arg
			625			630				635					640
Thr	Trp	Thr	Cys	Ser	His	Arg	Pro	Gly	Thr	Ala	Pro	Ser	Leu	His	Pro
			645						650						655
Gly	Leu	Arg	Ala	Pro	Leu	Pro	Cys	Trp	Pro	Gln	Pro	Cys	Trp	Gly	Ser
			660					665					670		
Pro	Pro	Gly	Gln	Glu	Gln	Ala	Arg	Val	Ile	Pro	Val	Pro	Pro	Gln	Glu
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<210> 145

<211> 2135

<212> DNA

<213> Homo sapiens

<400> 145

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<210> 146

<211> 630

<212> PRT

<213> Homo sapiens

<400> 146

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			20					25					30		
Pro	Ser	Arg	Thr	Leu	Ala	Gly	Glu	Thr	Gly	Gln	Glu	Ala	Ala	Pro	Leu
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Asp	Gly	Val	Leu	Ala	Asn	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg	
	50				55				60						
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu
65				70					75					80	
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85				90					95		
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
		100					105						110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
	115						120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135				140					
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
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Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu
			165					170						175	
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
		180					185						190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
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Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
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Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
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Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
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Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260					265						270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
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Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
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Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
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Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
			325					330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
		340					345						350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355				360						365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375					380				

Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
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			405						410					415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
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Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr
	435					440					445				
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln
465					470				475						480
Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn
			485					490						495	
Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro
		500						505					510		
Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
	515						520					525			
Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala	Val	Leu	Pro	Leu	Thr	Val
	530					535					540				
Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His	Val	Glu	Gly	Leu	Lys	Ala
545					550				555						560
Glu	Glu	Arg	His	Arg	Pro	Val	Arg	Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln
			565					570						575	
Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn
		580					585					590			
Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser	Val	Gln	Glu	Ala	Leu	Ser	Gly	Thr
	595					600					605				
Pro	Cys	Leu	Leu	Gly	Pro	Gly	Pro	Val	Leu	Thr	Val	Leu	Ala	Leu	Leu
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Leu	Ala	Ser	Thr	Leu	Ala										
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<210> 147

<211> 2105

<212> DNA

<213> Homo sapiens

<400> 147

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<210> 148

<211> 620

<212> PRT

<213> Homo sapiens

<400> 148

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          20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
          35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
          50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
          65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
          85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
          100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
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Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
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Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
          145          150          155          160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
          165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
          180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
          195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
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Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
          225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
          245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
          260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile

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Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met		
325	330	335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu		
340	345	350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val		
355	360	365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile		
370	375	380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu		
385	390	395
Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu		
405	410	415
Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln		
420	425	430
Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr		
435	440	445
Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser		
450	455	460
Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln		
465	470	475
Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn		
485	490	495
Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro		
500	505	510
Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu		
515	520	525
Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val		
530	535	540
Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala		
545	550	555
Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln		
565	570	575
Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn		
580	585	590
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<210> 149

<211> 2193

<212> DNA

<213> Homo sapiens

<400> 149

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cccgaggacc tggacgccct cccattggac ctgctgctat tcctcaacc agatgcgttc 480

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<210> 150

<211> 694

<212> PRT

<213> Homo sapiens

<400> 150

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20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100         105         110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115         120         125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130         135         140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145         150         155         160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165         170         175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu

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Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser		
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Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile		
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			405						410					415			
Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln	Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr		
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Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser	Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp		
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			485						490					495			
Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser		
			500					505					510				
Gln	Gln	Asn	Val	Ser	Met	Asp	Leu	Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr		
		515					520					525					
Asp	Ala	Val	Leu	Pro	Leu	Thr	Val	Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly		
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 Val Ile Pro Val Pro Pro Gln Glu Asn Ser Arg Ser Val Asn Gly Asn
 675 680 685
 Met Pro Pro Ala Asp Thr
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 <211> 2081
 <212> DNA
 <213> Homo sapiens

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<210> 152
 <211> 612
 <212> PRT
 <213> Homo sapiens

<400> 152
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Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser
 500 505 510
 Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr
 515 520 525
 Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly
 530 535 540
 Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg
 545 550 555 560
 Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu
 565 570 575
 Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser
 580 585 590
 Val Gln Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala
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 Ser Thr Leu Ala
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<210> 153

<211> 2111

<212> DNA

<213> Homo sapiens

<400> 153

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2111

<210> 154

<211> 622

<212> PRT

<213> Homo sapiens

<400> 154

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          20           25           30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
          35           40           45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
 50           55           60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65           70           75           80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
          85           90           95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
          100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
          115          120          125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
          130          135          140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
          145          150          155          160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
          165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
          180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
          195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
          210          215          220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
          225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
          245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
          260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
          275          280          285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
          290          295          300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
          305          310          315          320
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
          325          330          335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
          340          345          350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
          355          360          365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
          370          375          380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
          385          390          395          400
Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp

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Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr	Leu	Cys	Ser	Leu	Ser	Pro	Glu
		435					440					445		
Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser	Ile	Trp	Ala	Val	Arg	Pro	Gln
		450				455					460			
Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln	Leu	Asp	Val	Leu	Tyr	Pro	Lys
465					470				475					480
Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn	Gly	Ser	Glu	Tyr	Phe	Val	Lys
			485						490					495
Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro	Thr	Glu	Asp	Leu	Lys	Ala	Leu
			500					505					510	
Gln	Gln	Asn	Val	Ser	Met	Asp	Leu	Ala	Thr	Phe	Met	Lys	Leu	Arg
		515					520					525		
Asp	Ala	Val	Leu	Pro	Leu	Thr	Val	Ala	Glu	Val	Gln	Lys	Leu	Gly
		530				535					540			
Pro	His	Val	Glu	Gly	Leu	Lys	Ala	Glu	Glu	Arg	His	Arg	Pro	Val
545					550					555				560
Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln	Asp	Asp	Leu	Asp	Thr	Leu	Gly
			565					570						575
Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn	Gly	Tyr	Leu	Val	Leu	Asp	Leu
			580					585					590	
Val	Gln	Glu	Ala	Leu	Ser	Gly	Thr	Pro	Cys	Leu	Leu	Gly	Pro	Gly
		595				600						605		
Val	Leu	Thr	Val	Leu	Ala	Leu	Leu	Leu	Ala	Ser	Thr	Leu	Ala	
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<210> 155

<211> 1721

<212> DNA

<213> Homo sapiens

<400> 155

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<210> 156

<211> 515

<212> PRT

<213> Homo sapiens

<400> 156

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 20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115          120          125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130          135          140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145          150          155          160
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Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
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Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
195          200          205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
210          215          220
Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
225          230          235          240
Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
245          250          255
His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
260          265          270
Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
275          280          285
Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
290          295          300
Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
305          310          315          320
Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
325          330          335
Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
340          345          350
Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
355          360          365
Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr

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Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala				
	420		425	430
Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg				
	435		440	445
Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His				
	450		455	460
Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro				
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Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn				
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Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser				
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Ala Asn Leu				
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<210> 157

<211> 4139

<212> DNA

<213> Homo sapiens

<400> 157

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<210> 158

<211> 1255

<212> PRT

<213> Homo sapiens

<400> 158

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Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro

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Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
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Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
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Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			660					665						670	
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		675					680					685			
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Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
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Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			740					745					750		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		755					760					765			
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		770					775					780			
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				805					810					815	
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			820					825					830		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
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Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				885					890					895	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			900					905					910		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		915					920					925			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
		930					935					940			
Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser
		945			950					955					960
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			980					985					990		
Ser	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His
		995					1000					1005			
Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Ser	Val	Pro	Pro
		1010					1015					1020			
Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val
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Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser
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Ile	Ser	Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	
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Phe	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	
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Gln	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	
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Arg	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	
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Ser	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	
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<210> 159

<211> 2627

<212> DNA

<213> Homo sapiens

<400> 159

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<210> 160

<211> 700

<212> PRT

<213> Homo sapiens

<400> 160

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Lys Trp Thr His Glu Glu Asp Glu Gln Leu Arg Ala Leu Val Arg Gln
 35          40          45
Phe Gly Gln Gln Asp Trp Lys Phe Leu Ala Ser His Phe Pro Asn Arg
 50          55          60
Thr Asp Gln Gln Cys Gln Tyr Arg Trp Leu Arg Val Leu Asn Pro Asp
 65          70          75          80
Leu Val Lys Gly Pro Trp Thr Lys Glu Glu Asp Gln Lys Val Ile Glu
 85          90          95
Leu Val Lys Lys Tyr Gly Thr Lys Gln Trp Thr Leu Ile Ala Lys His
100          105          110
Leu Lys Gly Arg Leu Gly Lys Gln Cys Arg Glu Arg Trp His Asn His
115          120          125
Leu Asn Pro Glu Val Lys Lys Ser Cys Trp Thr Glu Glu Glu Asp Arg
130          135          140
Ile Ile Cys Glu Ala His Lys Val Leu Gly Asn Arg Trp Ala Glu Ile
145          150          155          160
Ala Lys Met Leu Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp
165          170          175
Asn Ser Thr Ile Lys Arg Lys Val Asp Thr Gly Gly Phe Leu Ser Glu
180          185          190
Ser Lys Asp Cys Lys Pro Pro Val Tyr Leu Leu Leu Glu Leu Glu Asp
195          200          205
Lys Asp Gly Leu Gln Ser Ala Gln Pro Thr Glu Gly Gln Gly Ser Leu
210          215          220
Leu Thr Asn Trp Pro Ser Val Pro Pro Thr Ile Lys Glu Glu Glu Asn
225          230          235          240
Ser Glu Glu Glu Leu Ala Ala Thr Thr Ser Lys Glu Gln Glu Pro
245          250          255
Ile Gly Thr Asp Leu Asp Ala Val Arg Thr Pro Glu Pro Leu Glu Glu
260          265          270

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Phe Pro Lys Arg Glu Asp Gln Glu Gly Ser Pro Pro Glu Thr Ser Leu
 275 280 285
 Pro Tyr Lys Trp Val Val Glu Ala Ala Asn Leu Leu Ile Pro Ala Val
 290 295 300
 Gly Ser Ser Leu Ser Glu Ala Leu Asp Leu Ile Glu Ser Asp Pro Asp
 305 310 315 320
 Ala Trp Cys Asp Leu Ser Lys Phe Asp Leu Pro Glu Glu Pro Ser Ala
 325 330 335
 Glu Asp Ser Ile Asn Asn Ser Leu Val Gln Leu Gln Ala Ser His Gln
 340 345 350
 Gln Gln Val Leu Pro Pro Arg Gln Pro Ser Ala Leu Val Pro Ser Val
 355 360 365
 Thr Glu Tyr Arg Leu Asp Gly His Thr Ile Ser Asp Leu Ser Arg Ser
 370 375 380
 Ser Arg Gly Glu Leu Ile Pro Ile Ser Pro Ser Thr Glu Val Gly Gly
 385 390 395 400
 Ser Gly Ile Gly Thr Pro Pro Ser Val Leu Lys Arg Gln Arg Lys Arg
 405 410 415
 Arg Val Ala Leu Ser Pro Val Thr Glu Asn Ser Thr Ser Leu Ser Phe
 420 425 430
 Leu Asp Ser Cys Asn Ser Leu Thr Pro Lys Ser Thr Pro Val Lys Thr
 435 440 445
 Leu Pro Phe Ser Pro Ser Gln Phe Leu Asn Phe Trp Asn Lys Gln Asp
 450 455 460
 Thr Leu Glu Leu Glu Ser Pro Ser Leu Thr Ser Thr Pro Val Cys Ser
 465 470 475 480
 Gln Lys Val Val Val Thr Thr Pro Leu His Arg Asp Lys Thr Pro Leu
 485 490 495
 His Gln Lys His Ala Ala Phe Val Thr Pro Asp Gln Lys Tyr Ser Met
 500 505 510
 Asp Asn Thr Pro His Thr Pro Thr Pro Phe Lys Asn Ala Leu Glu Lys
 515 520 525
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<211> 1938

<212> PRT

<213> Homo sapiens

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Tyr Lys Glu Gln Leu Gly Lys Leu Met Thr Thr Leu Arg Asn Thr Thr		655
	660	665
Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ser Gly		670
	675	680
		685

Lys	Leu	Asp	Ala	Phe	Leu	Val	Leu	Glu	Gln	Leu	Arg	Cys	Asn	Gly	Val
690						695					700				
Leu	Glu	Gly	Ile	Arg	Ile	Cys	Arg	Gln	Gly	Phe	Pro	Asn	Arg	Ile	Val
705					710					715					720
Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	Glu	Ile	Leu	Ala	Ala	Asn	Ala	Ile
				725					730					735	
Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	Gln	Ala	Cys	Ile	Leu	Met	Ile	Lys
			740					745					750		
Ala	Leu	Glu	Leu	Asp	Pro	Asn	Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Ile
			755				760					765			
Phe	Phe	Arg	Thr	Gly	Val	Leu	Ala	His	Leu	Glu	Glu	Glu	Arg	Asp	Leu
	770					775				780					
Lys	Ile	Thr	Asp	Val	Ile	Met	Ala	Phe	Gln	Ala	Met	Cys	Arg	Gly	Tyr
785					790					795					800
Leu	Ala	Arg	Lys	Ala	Phe	Ala	Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met
				805					810					815	
Lys	Val	Ile	Gln	Arg	Asn	Cys	Ala	Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp
			820					825					830		
Gln	Trp	Trp	Arg	Leu	Phe	Thr	Lys	Val	Lys	Pro	Leu	Leu	Gln	Val	Thr
	835						840						845		
Arg	Gln	Glu	Glu	Glu	Met	Gln	Ala	Lys	Glu	Asp	Glu	Leu	Gln	Lys	Thr
	850					855					860				
Lys	Glu	Arg	Gln	Gln	Lys	Ala	Glu	Asn	Glu	Leu	Lys	Glu	Leu	Glu	Gln
865					870					875					880
Lys	His	Ser	Gln	Leu	Thr	Glu	Glu	Lys	Asn	Leu	Leu	Gln	Glu	Gln	Leu
				885					890					895	
Gln	Ala	Glu	Thr	Glu	Leu	Tyr	Ala	Glu	Ala	Glu	Glu	Met	Arg	Val	Arg
			900					905					910		
Leu	Ala	Ala	Lys	Lys	Gln	Glu	Leu	Glu	Glu	Ile	Leu	His	Glu	Met	Glu
	915						920					925			
Ala	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Arg	Gly	Gln	Gln	Leu	Gln	Ala	Glu
	930					935					940				
Arg	Lys	Lys	Met	Ala	Gln	Gln	Met	Leu	Asp	Leu	Glu	Glu	Gln	Leu	Glu
945					950					955					960
Glu	Glu	Glu	Ala	Ala	Arg	Gln	Lys	Leu	Gln	Leu	Glu	Lys	Val	Thr	Ala
				965					970					975	
Glu	Ala	Lys	Ile	Lys	Lys	Leu	Glu	Asp	Glu	Ile	Leu	Val	Met	Asp	Asp
			980					985					990		
Gln	Asn	Asn	Lys	Leu	Ser	Lys	Glu	Arg	Lys	Leu	Leu	Glu	Glu	Arg	Ile
	995						1000						1005		
Ser	Asp	Leu	Thr	Thr	Asn	Leu	Ala	Glu	Glu	Glu	Glu	Lys	Ala	Lys	Asn
	1010					1015						1020			
Leu	Thr	Lys	Leu	Lys	Asn	Lys	His	Glu	Ser	Met	Ile	Ser	Glu	Leu	Glu
1025					1030					1035					1040
Val	Arg	Leu	Lys	Lys	Glu	Glu	Lys	Ser	Arg	Gln	Glu	Leu	Glu	Lys	Leu
				1045					1050					1055	
Lys	Arg	Lys	Leu	Glu	Gly	Asp	Ala	Ser	Asp	Phe	His	Glu	Gln	Ile	Ala
			1060					1065					1070		
Asp	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Lys	Met	Gln	Leu	Ala	Lys	Lys
	1075						1080					1085			
Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	Ala	Arg	Leu	Asp	Asp	Glu	Ile	Ala
	1090					1095					1100				
Gln	Lys	Asn	Asn	Ala	Leu	Lys	Lys	Ile	Arg	Glu	Leu	Glu	Gly	His	Ile
1105					1110					1115					1120
Ser	Asp	Leu	Gln	Glu	Asp	Leu	Asp	Ser	Glu	Arg	Ala	Ala	Arg	Asn	Lys
			1125						1130					1135	
Ala	Glu	Lys	Gln	Lys	Arg	Asp	Leu	Gly	Glu	Glu	Leu	Glu	Ala	Leu	Lys
			1140					1145					1150		
Thr	Glu	Leu	Glu	Asp	Thr	Leu	Asp	Ser	Thr	Ala	Thr	Gln	Gln	Glu	Leu

1155	1160	1165
Arg Ala Lys Arg Glu Gln Glu Val Thr Val Leu Lys Lys Ala Leu Asp		
1170	1175	1180
Glu Glu Thr Arg Ser His Glu Ala Gln Val Gln Glu Met Arg Gln Lys		
1185	1190	1195
His Ala Gln Ala Val Glu Glu Leu Thr Glu Gln Leu Glu Gln Phe Lys		1200
1205	1210	1215
Arg Ala Lys Ala Asn Leu Asp Lys Asn Lys Gln Thr Leu Glu Lys Glu		
1220	1225	1230
Asn Ala Asp Leu Ala Gly Glu Leu Arg Val Leu Gly Gln Ala Lys Gln		
1235	1240	1245
Glu Val Glu His Lys Lys Lys Lys Leu Glu Ala Gln Val Gln Glu Leu		
1250	1255	1260
Gln Ser Lys Cys Ser Asp Gly Glu Arg Ala Arg Ala Glu Leu Asn Asp		
1265	1270	1275
Lys Val His Lys Leu Gln Asn Glu Val Glu Ser Val Thr Gly Met Leu		
1285	1290	1295
Asn Glu Ala Glu Gly Lys Ala Ile Lys Leu Ala Lys Asp Val Ala Ser		
1300	1305	1310
Leu Ser Ser Gln Leu Gln Asp Thr Gln Glu Leu Leu Gln Glu Glu Thr		
1315	1320	1325
Arg Gln Lys Leu Asn Val Ser Thr Lys Leu Arg Gln Leu Glu Glu Glu		
1330	1335	1340
Arg Asn Ser Leu Gln Asp Gln Leu Asp Glu Glu Met Glu Ala Lys Gln		
1345	1350	1355
Asn Leu Glu Arg His Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser		
1365	1370	1375
Lys Lys Lys Leu Gln Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu		
1380	1385	1390
Gly Lys Lys Arg Phe Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr		
1395	1400	1405
Glu Glu Lys Ala Ala Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg		
1410	1415	1420
Leu Gln Gln Glu Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg		
1425	1430	1435
Gln Leu Val Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu		
1445	1450	1455
Leu Ala Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp		
1460	1465	1470
Arg Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu		
1475	1480	1485
Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg		
1490	1495	1500
Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser Ser Lys		
1505	1510	1515
Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser Lys Arg Ala		
1525	1530	1535
Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Glu		
1540	1545	1550
Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn		
1555	1560	1565
Met Gln Ala Leu Lys Gly Gln Phe Glu Arg Asp Leu Gln Ala Arg Asp		
1570	1575	1580
Glu Gln Asn Glu Glu Lys Arg Arg Gln Leu Gln Arg Gln Leu His Glu		
1585	1590	1595
Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala Ala		
1605	1610	1615
Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu Gln		
1620	1625	1630

Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg
 1635 1640 1645
 Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala
 1650 1655 1660
 Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys
 1665 1670 1675 1680
 Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu
 1685 1690 1695
 Ala Ala Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu
 1700 1705 1710
 Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln
 1715 1720 1725
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu Glu
 1730 1735 1740
 Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg Val Arg
 1745 1750 1755 1760
 Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu
 1765 1770 1775
 Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg
 1780 1785 1790
 Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val
 1795 1800 1805
 Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala
 1810 1815 1820
 Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala
 1825 1830 1835 1840
 Thr Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu
 1845 1850 1855
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln Ala
 1860 1865 1870
 Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu Glu Glu
 1875 1880 1885
 Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg Lys Leu Gln
 1890 1895 1900
 Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met Gly Arg Glu
 1905 1910 1915 1920
 Val Asn Ala Leu Lys Ser Lys Leu Arg Gly Pro Pro Pro Gln Glu Thr
 1925 1930 1935
 Ser Gln

<210> 165

<211> 958

<212> DNA

<213> Homo sapiens

<400> 165

tctaaagctc agtggagctg ggtcatctca ggccttggct ccttgaactt ttggccgccca 60
 tgtgcttccc gaagtcctc tctgatgaca tgaagaagct gaaggcccga atggtaatgc 120
 tcctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180
 ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttggtgc caactctgcc 240
 tctcttcaca gcaccaggcc atagaaagat tttatgataa aatgcaaaat gcagaatcag 300
 gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360
 tggagacagt ggcggcttat tatgaggagc agcaccaga gctcactcct ctacttgaag 420
 aagaaagaga tggattacgg tgccgaggga acagatcccc tgtcccggat gttgaggatc 480
 ccgcaaccga ggagcctggg gagagctttt gtracaagggt catgagatgg ttccaggcca 540
 tgctgcagcg gctgcagacc tgggtggcacg gggttctggc ctgggtgaag gagaagggtg 600
 tggccctggt ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660

tgtcagagct cttcatgtcc tctttccagt cctacggagc cccacggggg gacaaggagg 720
 agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780
 tttgccctcc ccgtcaccgc gcaccacccc tgacccctcc ctcagctgtc ctgtgccccg 840
 ccctctcccg cacactcagt ccccctgcct ggcgttcctg ccgcagctct gacctgggtgc 900
 tgtcgccctg gcatcttaat aaaacctgct tatacttccc tggcagggag ataccatg 958

<210> 166

<211> 234

<212> PRT

<213> Homo sapiens

<400> 166

Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala
1				5					10					15	
Arg	Met	Val	Met	Leu	Leu	Pro	Thr	Ser	Ala	Gln	Gly	Leu	Gly	Ala	Trp
		20						25					30		
Val	Ser	Ala	Cys	Asp	Thr	Glu	Asp	Thr	Val	Gly	His	Leu	Gly	Pro	Trp
		35					40					45			
Arg	Asp	Lys	Asp	Pro	Ala	Leu	Trp	Cys	Gln	Leu	Cys	Leu	Ser	Ser	Gln
		50				55					60				
His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	Glu	Ser
65					70				75					80	
Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Asp	Phe
			85						90				95		
Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	Gln	His
			100					105					110		
Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	Arg	Cys
		115					120					125			
Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	Thr	Glu
		130				135					140				
Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asx	Lys	Val	Met	Arg	Trp	Phe	Gln	Ala
145					150					155				160	
Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala	Trp	Val
			165						170					175	
Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu	Trp	Lys
			180					185					190		
Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met	Ser	Ser
		195					200					205			
Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu	Thr	Pro
		210				215					220				
Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys						
225						230									

<210> 167

<211> 958

<212> DNA

<213> Homo sapiens

<400> 167

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 tgtgcttccc gaaggtcctc tctgatgaca tgaagaagct gaaggcccgga atggtaaatgc 120
 tctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180
 ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttgggtgc caactctgcc 240
 tctcttcaca gcaccaggcc atagaaaagat tttatgataa aatgcaaaat gcagaatcag 300
 gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360
 tggagacagt ggcggcttat tatgaggagc agcaccagga gctcactcct ctacttgaaa 420
 aagaaagaga tggattacgg tgccgaggca acagatcccc tgtcccggat gttgaggatc 480
 ccgcaaccga ggagcctggg gagagctttt gtgacaaggt catgagatgg ttccaggcca 540

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tgctgcagcg gctgcagacc tgggtggcacg gggttctggc ctgggtgaag gagaagggtg 600
tggccctggg ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660
tgtcagagct cttcatgtcc tctttccagt cctacggagc cccacggggg gacaaggagg 720
agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780
tttgcctctc ccgtcaccgc gcaccacccc tgaccctctc ctcagctgtc ctgtgccccg 840
ccctctcccg cacactcagt ccccctgcct ggcgttcctg ccgcagctct gacctgggtg 900
tgtgcgcttg gcatcttaat aaaacctgct tatacttccc tggcagggag ataccatg 958

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<210> 168

<211> 234

<212> PRT

<213> Homo sapiens

<400> 168

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Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1          5          10          15
Arg Met Val Met Leu Leu Pro Thr Ser Ala Gln Gly Leu Gly Ala Trp
20          25          30
Val Ser Ala Cys Asp Thr Glu Asp Thr Val Gly His Leu Gly Pro Trp
35          40          45
Arg Asp Lys Asp Pro Ala Leu Trp Cys Gln Leu Cys Leu Ser Ser Gln
50          55          60
His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser
65          70          75          80
Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe
85          90          95
Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His
100         105         110
Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys
115         120         125
Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu
130         135         140
Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala
145         150         155         160
Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala Trp Val
165         170         175
Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu Trp Lys
180         185         190
Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser
195         200         205
Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro
210         215         220
Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
225         230

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<210> 169

<211> 1005

<212> DNA

<213> Homo sapiens

<400> 169

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tgtgtgtgcta ttgtgtggat gccgcgcgtg tcttctcttc tttccagaga tggctaacag 60
gggccccgagc tatggcttaa gccgagaggt gcaggagaag atcgagcaga agtatgatgc 120
ggacctggag aacaagctgg tggactggat catcctgcag tgcgccgagg acatagagca 180
ccgcgccccc ggcagggcc attttcagaa atggttaatg gacgggacgg tcctgtgcaa 240
gctgataaat agtttatacc caccaggaca agagcccata cccaagatct cagagtcaaa 300
gatggctttt aagcagatgg agcaaatctc ccagttccta aaagctgcgg agacctatgg 360
tgtcagaacc accgacatct ttcagacggg ggatctatgg gaagggaagg acatggcagc 420

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tgtgcagagg accctgatgg ctttaggcag cgttgcagtc accaaggatg atggctgcta 480
tcggggagag ccatacctggt ttcacaggaa agcccagcag aatcgagag gcttttccga 540
ggagcagctt cgccagggaac agaacgtaat aggcctgcag atgggcagca acaagggagc 600
ctcccaggcg ggcatagacag ggtacgggat gccacggcag atcatgttag gacgcggcat 660
cctgcccctg gtagagagga cgaatgttcc acaccatggt ctctacgaaa aagaaatagt 720
tagtcacctt ctgaccttct cctctttctc aaagccttct gtccctgggt tttgcaagtg 780
ctgcatttcc gccgagaatc cgcgttgccct actgctgcca cctcctgttc atttagaact 840
atgcaaagac tccgcttccg ttttctgag ctccctcgggc cccagagtct ctgtttgatt 900
atttatttat ttatttattt atttgccaaa aattctctct ttcaacttat agaatgcacc 960
taataaagta attaagtctt gtggaaaaaa aaaaaaaaaa aaaaaa 1005

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<210> 170

<211> 282

<212> PRT

<213> Homo sapiens

<400> 170

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Met Ala Asn Arg Gly Pro Ser Tyr Gly Leu Ser Arg Glu Val Gln Glu
 1          5          10          15
Lys Ile Glu Gln Lys Tyr Asp Ala Asp Leu Glu Asn Lys Leu Val Asp
          20          25          30
Trp Ile Ile Leu Gln Cys Ala Glu Asp Ile Glu His Pro Pro Gly
          35          40          45
Arg Ala His Phe Gln Lys Trp Leu Met Asp Gly Thr Val Leu Cys Lys
          50          55          60
Leu Ile Asn Ser Leu Tyr Pro Pro Gly Gln Glu Pro Ile Pro Lys Ile
          65          70          75          80
Ser Glu Ser Lys Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
          85          90          95
Leu Lys Ala Ala Glu Thr Tyr Gly Val Arg Thr Thr Asp Ile Phe Gln
          100          105          110
Thr Val Asp Leu Trp Glu Gly Lys Asp Met Ala Ala Val Gln Arg Thr
          115          120          125
Leu Met Ala Leu Gly Ser Val Ala Val Thr Lys Asp Asp Gly Cys Tyr
          130          135          140
Arg Gly Glu Pro Ser Trp Phe His Arg Lys Ala Gln Gln Asn Arg Arg
          145          150          155          160
Gly Phe Ser Glu Glu Gln Leu Arg Gln Gly Gln Asn Val Ile Gly Leu
          165          170          175
Gln Met Gly Ser Asn Lys Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr
          180          185          190
Gly Met Pro Arg Gln Ile Met Leu Gly Arg Gly Ile Leu Pro Leu Val
          195          200          205
Glu Arg Thr Asn Val Pro His His Gly Leu Tyr Glu Lys Glu Ile Val
          210          215          220
Ser His Leu Leu Thr Phe Ser Ser Phe Ser Lys Pro Ser Val Pro Gly
          225          230          235          240
Phe Cys Lys Cys Cys Ile Ser Ala Glu Asn Pro Arg Cys Leu Leu Leu
          245          250          255
Pro Pro Pro Val His Leu Glu Leu Cys Lys Asp Ser Ala Ser Val Phe
          260          265          270
Leu Ser Ser Ser Gly Pro Arg Val Ser Val
          275          280

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<210> 171

<211> 942

<212> DNA

<213> Homo sapiens

<400> 171

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atgagaattg cagtgatttg cttttgcctc ctaggcatca cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagctttaca acaaataccc agatgctgtg 120
gccacatggc taaaccctga cccatctcag aagcagaatc tcctagcccc acagaatgct 180
gtgtcctctg aagaaaccaa tgacttttaa caagagaccc ttccaagtaa gtccaacgaa 240
agccatgacc acatggatga tatggatgat gaagatgatg atgaccatgt ggacagccag 300
gactccattg actcgaacga ctctgatgat gtagatgaca ctgatgattc tcaccagtct 360
gatgagtctc accattctga tgaatctgat gaactggtca ctgattttcc cacggacctg 420
ccagcaaccg aagttttcac tccagttgtc cccacagtag acacatatga tggccgaggt 480
gatagtgtgg tttatggact gaggtcaaaa tctaagaagt ttcgcagacc tgacatccag 540
taccctgatg ctacagacga gcacatcacc tcacacatgg aaagcgagga gttgaatgg 600
gcatacaagg ccatccccgt tgcccaggac ctgaacgcgc cttctgattg ggacagccgt 660
gggaaggaca gttatgaaac gagtcagctg gatgaccaga gtgctgaagc ccacagccac 720
aagcagtoaa gattatataa gcggaaagct aatgatgaga gcaatgagca ttccgatgtg 780
attgatagtc aggaactttc caaagtcagc cgtgaattcc acagccatga atttcacagc 840
catgaagata tgctggttgt agaccccaaa agtaaggaag aagataaaca cctgaaattt 900
cgtatttctc atgaattaga tagtgcactc tctgaggtca at 942

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<210> 172

<211> 314

<212> PRT

<213> Homo sapiens

<400> 172

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Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
1      5      10      15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
20      25      30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
35      40      45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
50      55      60
Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
65      70      75      80
Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
85      90      95
Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100     105     110
Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115     120     125
Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130     135     140
Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly
145     150     155     160
Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
165     170     175
Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu His Ile Thr Ser His
180     185     190
Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195     200     205
Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210     215     220
Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Ala His Ser His
225     230     235     240
Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245     250     255
His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260     265     270

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Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp
 275 280 285
 Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His
 290 295 300
 Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
 305 310

<210> 173
 <211> 1524
 <212> DNA
 <213> Homo sapiens

<400> 173
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 aacgccgacc aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta 120
 ggcatcacct gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag 180
 ctttacaaca aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag 240
 cagaatctcc tagccccaca gacccttcca agtaagtcca acgaaagcca tgaccacatg 300
 gatgatatgg atgatgaaga tgatgatgac catgtggaca gccaggactc cattgactcg 360
 aacgactctg atgatgtaga tgacactgat gattctcacc agtctgatga gtctcaccat 420
 tctgatgaat ctgatgaact ggctactgat tttcccacgg acctgccagc aaccgaagtt 480
 ttcactccag ttgtcccccac agtagacaca tatgatggcc gaggtgatag tgtggtttat 540
 ggactgaggt caaaatctaa gaagtttcgc agacctgaca tccagtaccc tgatgctaca 600
 gacgaggaca tcacctcaca catggaaagc gaggagttga atgggtgcata caaggccatc 660
 cccgttgccc aggacctgaa cgcgcttctt gattgggaca gccgtgggaa ggacagttat 720
 gaaacgagtc agctggatga ccagagtgtt gaaacccaca gccacaagca gtccagatta 780
 tataagcggg aagccaatga tgagagcaat gagcattccg atgtgattga tagtcaggaa 840
 ctttccaaag tcagccgtga attccacagc catgaatttc acagccatga agatattgctg 900
 gttgtagacc ccaaaagttaa ggaagaagat aaacacctga aatttcgtat ttctcatgaa 960
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 ctgagtttat tgggtgaatg tgtatctatt tgagtctgga aataactaat gtgtttgata 1140
 attagtttag tttgtggctt catggaaact ccctgtaaac taaaagcttc agggttatgt 1200
 ctatgttcat tctatagaag aaatgcaaac tatcactgta ttttaatat ttgtattctc 1260
 tcatgaatag aaatttatgt agaagcaaac aaaatacttt taccactta aaaagagaat 1320
 ataacatttt atgtcactat aatcttttgt tttttaagtt agtgtatatt ttgttgtgat 1380
 tatctttttg tgggtggaat aaatctttta tcttgaatgt aataagaatt tgggtggtgc 1440
 aattgcttat ttgttttccc acggttgtcc agcaattaat aaaacataac cttttttact 1500
 gcctaaaaaa aaaaaaaaaa aaaa 1524

<210> 174
 <211> 300
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1 5 10 15
 Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20 25 30
 Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35 40 45
 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
 50 55 60
 Asn Glu Ser His Asp His Met Asp Asp Met Asp Glu Asp Asp Asp
 65 70 75 80
 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
 85 90 95

```

Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
      100      105      110
Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
      115      120      125
Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
      130      135      140
Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
      145      150      155      160
Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
      165      170      175
Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
      180      185      190
Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
      195      200      205
Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
      210      215      220
Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
      225      230      235      240
Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
      245      250      255
Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
      260      265      270
Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
      275      280      285
Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn
      290      295      300

```

<210> 175
 <211> 861
 <212> DNA
 <213> Homo sapiens

```

<400> 175
atgagaattg cagtgatttg cttttgcctc ctaggcacat cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagaatgctg tgtcctctga agaaaccaat 120
gacttttaaac aagagaccct tccaagtaag tccaacgaaa gccatgacca catggatgat 180
atggatgatg aagatgatga tgaccatgtg gacagccagg actccattga ctcgaacgac 240
tctgatgatg tagatgacac tgatgattct caccagtctg atgagtctca ccattctgat 300
gaatctgatg aactggtcac tgattttccc acggacctgc cagcaaccga agttttcact 360
ccagttgtcc ccacagtaga cacatatgat ggccgagggtg atagtgtggt ttatggactg 420
aggtcaaaat ctaagaagtt tcgcagacct gacatccagt accctgatgc tacagacgag 480
cacatcacct cacacatgga aagcgaggag ttgaatggtg catacaaggc catccccgtt 540
gcccgaggacc tgaacgcgcc ttctgattgg gacagccgtg ggaaggacag ttatgaaacg 600
agtcagctgg atgaccagag tgctgaagcc cacagccaca agcagtccag attatataag 660
cgaaaagcta atgatgagag caatgagcat tccgatgtga ttgatagtca ggaactttcc 720
aaagtcagcc gtgaattcca cagccatgaa ttccacagcc atgaagatat gctggttgta 780
gacccccaaa gtaaggaaga agataaacac ctgaaatttc gtattttctca tgaattagat 840
agtgcattct ctgaggtcaa t                                     861

```

<210> 176
 <211> 287
 <212> PRT
 <213> Homo sapiens

```

<400> 176
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
  1           5           10          15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Asn

```

```
<210> 177
<211> 3213
<212> DNA
<213> Homo sapiens
```

<400>	177					
agagactcaa	gatgattccc	tttttaccca	tgttttctct	actattgctg	cttattgtta	60
acctataaaa	cgccacaacat	cattatgaca	agatcctggc	tcatagtcgt	atcaggggtc	120
gggaccaagg	cccaaatgtc	tgtgcccttc	aacagatttt	gggcacaaaa	aagaaatact	180
tcagcacttg	taagaacttg	tataaaaagt	ccatctgtgg	acagaaaaacg	actgttttat	240
atgaattgtg	ccttggttat	atgagaattg	aaggaatgaa	aggctgccca	cgacttttgc	300
ccattgacca	tgtttatggc	actctgggca	tcgtgggagc	caccacaacg	cagcgctatt	360
ctgacgcctc	aaaactgagg	gaggagatcg	agggaaaggg	atccttcact	tactttgcac	420
cgagtaatga	ggcttgggac	aacttggtat	ctgatatccg	tagaggtttg	gagagcaacg	480
tgaatgttga	attactgaat	gctttacata	gtcacatgat	taataagaga	atgttgacca	540
aggactttaa	aaatggcatg	attattcctt	caatgtataa	caatttgggg	cttttcatta	600
accattatoc	taatgggggt	gtcactgtta	atttgtctcg	aatcatccat	gggaaccaga	660
ttgcaacaaa	tggtgttgtc	catgtcattg	accgtgtgct	tacacaqaat	ggtagctcaa	720
ttcaagactt	cattgaagca	gaagatgacc	tttcatcttt	tagagcagct	gccatcacat	780
cggacatat	ggaggccctt	ggaagagacg	gtcacttcac	actctttgct	cccaccaatg	840
aggcttttga	gaaacttcca	cgagggtgcc	tagaaagggt	catgggagac	aaagtggctt	900
ccgaagctct	tatgaagtac	cacactctaa	atactctcca	gtgttctgag	tctattatgg	960
gaggagcagt	ctttgagacg	ctggaaggaa	atacaattga	gataggatgt	gacggtgaca	1020
qtataacagt	aaatggaatc	aaaatggtga	acaaaaagga	tattgtgaca	aataatqdtg	1080

```

tgatccattt gattgatcag gtcctaattc ctgattctgc caaacaagtt attgagctgg 1140
ctggaaaaca gcaaaccacc ttcacggatc ttgtggccca attaggcttg gcatctgctc 1200
tgaggccaga tggagaatac actttgctgg cacctgtgaa taatgcattt tctgatgata 1260
ctctcagcat gggtcagcgc ctcccttaaat taattctgca gaatcacata ttgaaagtaa 1320
aagttggcct taatgagctt tacaacgggc aaatactgga aaccatcgga ggcaaacagc 1380
tcagagtctt cgtatatcgt acagctgtct gcattgaaaa ttcatgcatg gagaaagggg 1440
gtaagcaagg gagaaacggt gcgattcaca tattccgcga gatcatcaag ccagcagaga 1500
aatccctoca tgaaaagtta aaacaagata agcgctttag caccttcctc agcctacttg 1560
aagctgcaga cttgaaagag ctccctgacac aaacctggaga ctggacatta tttgtgccaa 1620
ccaatgatgc ttttaaggga atgactagag aagaaaaaga aattctgata cgggacaaaa 1680
atgctcttca aaacatcatt ctttatcacc tgacaccagg agttttcatt ggaaaaggat 1740
ttgaacctgg tgttactaac attttaaaga ccacacaagg aagcaaaatc tttctgaaag 1800
aagtaaataa tacacttctg gtgaatgaat tgaaatcaaa agaactctgac atcatgacaa 1860
caaattggtg aattcatggt gtagataaac tcctctatcc agcagacaca cctgttggaa 1920
atgatcaact gctggaaata ctttaataaat taatcaaaata catccaaatt aagtttgttc 1980
gtggttagcac cttcaaagaa atccccgtga ctgtctatac aactaaaatt ataaccaaag 2040
ttgtggaacc aaaaattaaa gtgattgaag gcagtcttca gcctattatc aaaactgaag 2100
gacccacact aacaaaagtc aaaaattgaag gtgaacctga attcagactg attaaagaag 2160
gtgaaacaat aactgaagtg atccatggag agccaattat taaaaaatac accaaaatca 2220
ttgatggagt gcctgtggaa ataactgaaa aagagacacg agaagaacga atcattacag 2280
gtcctgaaat aaaatacact aggatttcta ctggaggtgg agaaacagaa gaaactctga 2340
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tgtggagtta gcctcctgtg gtaaaggaat tgaagaaaat ataacacctt acaccttttt 2760
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ccagattcat tacaattcaa atcgaagagt tgtgaactgt tatcccattg aaaagaccga 2880
gccttgtatg tatgttatgg atacataaaa tgcacgcaag ccattatctc tccatgggaa 2940
gctaagttat aaaaataggt gcttggtgta caaaactttt tatatcaaaa ggctttgcac 3000
atttctatat gagtgggttt actggtaaata tatgttattt tttacaacta attttgtact 3060
ctcagaatgt ttgtcatatg cttcttgcaa tgcataattt ttaatctcaa acgtttcaat 3120
aaaaccattt ttcagatata aagagaatta cttcaaattg agtaattcag aaaaactcaa 3180
gatttaagtt aaaaagtggt ttggacttgg gaa 3213

```

<210> 178

<211> 836

<212> PRT

<213> Homo sapiens

<400> 178

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
1           5           10           15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20           25           30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35           40           45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50           55           60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65           70           75           80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85           90           95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100          105          110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115          120          125

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	595		600		605	
Ser	Lys	Glu	Ser	Asp	Ile	Met
	610					615
Asp	Lys	Leu	Leu	Tyr	Pro	Ala
	625					630
Leu	Glu	Ile	Leu	Asn	Lys	Leu
						645
Arg	Gly	Ser	Thr	Phe	Lys	Glu
						660
Ile	Ile	Thr	Lys	Val	Val	Glu
						675
Leu	Gln	Pro	Ile	Ile	Lys	Thr
						690
Ile	Glu	Gly	Glu	Pro	Glu	Phe
						705
Thr	Glu	Val	Ile	His	Gly	Glu
						725
Ile	Asp	Gly	Val	Pro	Val	Glu
						740
Arg	Ile	Ile	Thr	Gly	Pro	Glu
						755
Gly	Gly	Glu	Thr	Glu	Glu	Thr
						770
Thr	Lys	Val	Thr	Lys	Phe	Ile
						785
Asp	Glu	Glu	Ile	Lys	Arg	Leu
						805
Leu	Gln	Ala	Asn	Lys	Lys	Val
						820
Gly	Arg	Ser	Gln			
						835

<210> 179

<211> 3077

<212> DNA

<213> Homo sapiens

<400> 179

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ttgctgctta ttgttaaccc tataaacgcc aacaatcatt atgacaagat cttggctcat 120
agtcgtatca ggggtcggga ccaaggccca aatgtctgtg cccttcaaca gattttgggc 180
acaaaaaaga aatacttcag cacttgtaag aactgggata aaaagtccat ctgtggacag 240
aaaacgactg ttttatatga atgttgccct gggttatatga gaattggaagg aatgaaaggc 300
tgcccagcag ttttgcccat tgaccatggt tatggcactc tgggcatcgt gggagccacc 360
acaacgcagc gctattctga cgcctcaaaa ctgagggagg agatcgaggg aaagggatcc 420
ttcacttact ttgcaccgag taatgagggt tgggacaact tggattctga tatccgtaga 480
ggtttgagga gcaacgtgaa tgttgaatta ctgaatgctt tacatagtca catgattaat 540
aagagaatgt tgaccaagga cttaaaaaat ggcattgatta ttccttcaat gtataacaat 600
ttggggcttt tcattaacca ttatcctaatt ggggttggtc ctggttaattg tgctcgaatc 660
atccatggga accagattgc aacaaatggt gttgtccatg tcattgaccg tgtgcttaca 720
caaattggta cctcaattca agacttcatt gaagcagaag atgacctttc atcttttaga 780
gcagctgcc aacatcgga catattggag gcccttggaa gagacggtca cttcacactc 840
tttgctccca ccaatgaggc ttttgagaaa cttccacgag gtgtcctaga aagggtcatg 900
ggagacaaag tggcttccga agctcttatg aagtaccaca tcttaaatac tctccagtgt 960
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gtgacaaata atggtgtgat ccatttgatt gatcaggtcc taattcctga ttctgccaaa 1140
caagttattg agctggctgg aaaacagcaa accaccttca cggatcttgt ggcccaatta 1200

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ggcttggcat ctgctctgag gccagatgga gaatacaactt tgctggcacc tgtgaataat 1260
gcatttttctg atgatactct cagcatgggtt cagcgccctcc tttaaattaat tctgcagaat 1320
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tttggaacttg ggaacag 3077

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<210> 180

<211> 779

<212> PRT

<213> Homo sapiens

<400> 180

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
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Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20           25           30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35           40           45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50           55           60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65           70           75           80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85           90           95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100          105          110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115          120          125
Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130          135          140
Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
145          150          155          160

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Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	Asn	Lys	Arg	Met	Leu	Thr
				165					170					175	
Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	Ser	Met	Tyr	Asn	Asn	Leu
			180					185					190		
Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	Val	Val	Thr	Val	Asn	Cys
		195					200					205			
Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	Thr	Asn	Gly	Val	Val	His
	210				215						220				
Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	Thr	Ser	Ile	Gln	Asp	Phe
225				230						235					240
Ile	Glu	Ala	Glu	Asp	Asp	Leu	Ser	Ser	Phe	Arg	Ala	Ala	Ala	Ile	Thr
			245						250					255	
Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	Gly	His	Phe	Thr	Leu	Phe
		260						265					270		
Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	Pro	Arg	Gly	Val	Leu	Glu
	275						280					285			
Arg	Phe	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	Ala	Leu	Met	Lys	Tyr	His
	290				295						300				
Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	Ile	Met	Gly	Gly	Ala	Val
305				310						315					320
Phe	Glu	Thr	Leu	Glu	Gly	Asn	Thr	Ile	Glu	Ile	Gly	Cys	Asp	Gly	Asp
			325						330					335	
Ser	Ile	Thr	Val	Asn	Gly	Ile	Lys	Met	Val	Asn	Lys	Lys	Asp	Ile	Val
		340						345					350		
Thr	Asn	Asn	Gly	Val	Ile	His	Leu	Ile	Asp	Gln	Val	Leu	Ile	Pro	Asp
	355						360					365			
Ser	Ala	Lys	Gln	Val	Ile	Glu	Leu	Ala	Gly	Lys	Gln	Gln	Thr	Thr	Phe
	370				375						380				
Thr	Asp	Leu	Val	Ala	Gln	Leu	Gly	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Asp
385				390						395					400
Gly	Glu	Tyr	Thr	Leu	Leu	Ala	Pro	Val	Asn	Asn	Ala	Phe	Ser	Asp	Asp
			405					410						415	
Thr	Leu	Ser	Met	Val	Gln	Arg	Leu	Leu	Lys	Leu	Ile	Leu	Gln	Asn	His
		420						425					430		
Ile	Leu	Lys	Val	Lys	Val	Gly	Leu	Asn	Glu	Leu	Tyr	Asn	Gly	Gln	Ile
	435						440					445			
Leu	Glu	Thr	Ile	Gly	Gly	Lys	Gln	Leu	Arg	Val	Phe	Val	Tyr	Arg	Thr
	450				455						460				
Ala	Val	Cys	Ile	Glu	Asn	Ser	Cys	Met	Glu	Lys	Gly	Ser	Lys	Gln	Gly
465					470					475					480
Arg	Asn	Gly	Ala	Ile	His	Ile	Phe	Arg	Glu	Ile	Ile	Lys	Pro	Ala	Glu
			485						490					495	
Lys	Ser	Leu	His	Glu	Lys	Leu	Lys	Gln	Asp	Lys	Arg	Phe	Ser	Thr	Phe
		500						505					510		
Leu	Ser	Leu	Leu	Glu	Ala	Ala	Asp	Leu	Lys	Glu	Leu	Leu	Thr	Gln	Pro
		515					520					525			
Gly	Asp	Trp	Thr	Leu	Phe	Val	Pro	Thr	Asn	Asp	Ala	Phe	Lys	Gly	Met
	530				535						540				
Thr	Ser	Glu	Glu	Lys	Glu	Ile	Leu	Ile	Arg	Asp	Lys	Asn	Ala	Leu	Gln
545				550						555					560
Asn	Ile	Ile	Leu	Tyr	His	Leu	Thr	Pro	Gly	Val	Phe	Ile	Gly	Lys	Gly
			565						570					575	
Phe	Glu	Pro	Gly	Val	Thr	Asn	Ile	Leu	Lys	Thr	Thr	Gln	Gly	Ser	Lys
		580					585						590		
Ile	Phe	Leu	Lys	Glu	Val	Asn	Asp	Thr	Leu	Leu	Val	Asn	Glu	Leu	Lys
		595					600					605			
Ser	Lys	Glu	Ser	Asp	Ile	Met	Thr	Thr	Asn	Gly	Val	Ile	His	Val	Val
	610					615					620				
Asp	Lys	Leu	Leu	Tyr	Pro	Ala	Asp	Thr	Pro	Val	Gly	Asn	Asp	Gln	Leu

625		630		635		640
Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val						
		645		650		655
Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Lys Pro Ile						
		660		665		670
Ile Lys Lys Tyr Thr Lys Ile Ile Asp Gly Val Pro Val Glu Ile Thr						
		675		680		685
Glu Lys Glu Thr Arg Glu Glu Arg Ile Ile Thr Gly Pro Glu Ile Lys						
		690		695		700
Tyr Thr Arg Ile Ser Thr Gly Gly Gly Glu Thr Glu Glu Thr Leu Lys						
705		710		715		720
Lys Leu Leu Gln Glu Glu Val Thr Lys Val Thr Lys Phe Ile Glu Gly						
		725		730		735
Gly Asp Gly His Leu Phe Glu Asp Glu Glu Ile Lys Arg Leu Leu Gln						
		740		745		750
Gly Asp Thr Pro Val Arg Lys Leu Gln Ala Asn Lys Lys Val Gln Gly						
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Ser Arg Arg Arg Leu Arg Glu Gly Arg Ser Gln						
770		775				

<210> 181
 <211> 2088
 <212> DNA
 <213> Homo sapiens

<400> 181

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 ccactattta ataaaagtaa tagaatcaga aaaaaaaaaa aaaaaaaaaa 2088

<210> 182

<211> 334

<212> PRT

<213> Homo sapiens

<400> 182

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Thr	Pro	Pro	Pro	Gly	Gly	Lys	Asp	Arg	Glu	Ala	Phe	Glu	Ala	Glu	Tyr
			20					25					30		
Arg	Leu	Gly	Pro	Leu	Leu	Gly	Lys	Gly	Gly	Phe	Gly	Thr	Val	Phe	Ala
		35					40					45			
Gly	His	Arg	Leu	Thr	Asp	Arg	Leu	Gln	Val	Ala	Ile	Lys	Val	Ile	Pro
	50					55					60				
Arg	Asn	Arg	Val	Leu	Gly	Trp	Ser	Pro	Leu	Ser	Asp	Ser	Val	Thr	Cys
	65				70					75					80
Pro	Leu	Glu	Val	Ala	Leu	Leu	Trp	Lys	Val	Gly	Ala	Gly	Gly	Gly	His
				85					90					95	
Pro	Gly	Val	Ile	Arg	Leu	Leu	Asp	Trp	Phe	Glu	Thr	Gln	Glu	Gly	Phe
			100					105					110		
Met	Leu	Val	Leu	Glu	Arg	Pro	Leu	Pro	Ala	Gln	Asp	Leu	Phe	Asp	Tyr
		115					120					125			
Ile	Thr	Glu	Lys	Gly	Pro	Leu	Gly	Glu	Gly	Pro	Ser	Arg	Cys	Phe	Phe
	130					135					140				
Gly	Gln	Val	Val	Ala	Ala	Ile	Gln	His	Cys	His	Ser	Arg	Gly	Val	Val
	145					150				155					160
His	Arg	Asp	Ile	Lys	Asp	Glu	Asn	Ile	Leu	Ile	Asp	Leu	Arg	Arg	Gly
				165					170					175	
Cys	Ala	Lys	Leu	Ile	Asp	Phe	Gly	Ser	Gly	Ala	Leu	Leu	His	Asp	Glu
			180					185					190		
Pro	Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr	Ser	Pro	Pro	Glu	Trp
		195					200					205			
Ile	Ser	Arg	His	Gln	Tyr	His	Ala	Leu	Pro	Ala	Thr	Val	Trp	Ser	Leu
	210					215					220				
Gly	Ile	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp	Ile	Pro	Phe	Glu	Arg
	225				230					235					240
Asp	Gln	Glu	Ile	Leu	Glu	Ala	Glu	Leu	His	Phe	Pro	Ala	His	Val	Ser
				245					250					255	
Pro	Asp	Cys	Cys	Ala	Leu	Ile	Arg	Arg	Cys	Leu	Ala	Pro	Lys	Pro	Ser
		260						265					270		
Ser	Arg	Pro	Ser	Leu	Glu	Glu	Ile	Leu	Leu	Asp	Pro	Trp	Met	Gln	Thr
		275					280					285			
Pro	Ala	Glu	Asp	Val	Thr	Pro	Gln	Pro	Leu	Gln	Arg	Arg	Pro	Cys	Pro
	290					295					300				
Phe	Gly	Leu	Val	Leu	Ala	Thr	Leu	Ser	Leu	Ala	Trp	Pro	Gly	Leu	Ala
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Pro	Asn	Gly	Gln	Lys	Ser	His	Pro	Met	Ala	Met	Ser	Gln	Gly		
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<210> 183

<211> 2304

<212> DNA

<213> Homo sapiens

<400> 183

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<210> 184

<211> 431

<212> PRT

<213> Homo sapiens

<400> 184

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Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20          25          30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35          40          45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50          55          60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65          70          75          80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85          90          95

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Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
 180 185 190
 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205
 Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220
 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240
 Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255
 Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270
 His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320
 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335
 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350
 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415
 Pro Trp Ile Arg Ser His Thr Lys Glu Asn Gly Leu Ala Leu
 420 425 430

<210> 185

<211> 2123

<212> DNA

<213> Homo sapiens

<400> 185

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 gagccgcaca agaggaggaa agccctgact gagcctgagg cccgatacta cctacggcaa 540

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<210> 186

<211> 603

<212> PRT

<213> Homo sapiens

<400> 186

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20      25      30
Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
35      40      45
Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
50      55      60
Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
65      70      75      80
Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
85      90      95
Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
100     105     110
Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
115     120     125
Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Pro His Lys Arg
130     135     140
Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
145     150     155     160
Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
165     170     175
Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
180     185     190
Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys

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cgaactagaa atagaaccac caagagtaga agtcgaagca gtagcagtag cagttctagt 1860
agcagttcaa ccagtagcag cagtggaggt agttccagca gtggaagtag tagcagtcgc 1920
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actagtagta gtagtgagag tagaagtcgg agtagggggc ggggacataa tagagataga 2040
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aaatcttcaa aaggtgtag tagtagagat acaaaaggat caaaggataa gaattcccg 2160
tccgacagaa agaggtctat atcagagagt agtcgatcag gcaaaagatc ttcaagaagt 2220
gaaagagacc gaaaatcaga caggaaagac aaaaggcgtt aatggaagaa gccaggcttt 2280
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gaggatgctg ccttaagaat tgcatgttgt aaaaaatctt tttggaagat acagactgtt 2400
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<210> 188

<211> 743

<212> PRT

<213> Homo sapiens

<400> 188

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Met Ala Val Ala Val Arg Thr Leu Gln Glu Gln Leu Glu Lys Ala Lys
  1             5             10             15
Glu Ser Leu Lys Asn Val Asp Glu Asn Ile Arg Lys Leu Thr Gly Arg
      20             25             30
Asp Pro Asn Asp Val Arg Pro Ile Gln Ala Arg Leu Leu Ala Leu Ser
      35             40             45
Gly Pro Gly Gly Gly Arg Gly Arg Gly Ser Leu Leu Leu Arg Arg Gly
      50             55             60

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Phe	Ser	Asp	Ser	Gly	Gly	Pro	Pro	Ala	Lys	Gln	Arg	Asp	Leu	Glu	Gly
65					70					75					80
Ala	Val	Ser	Arg	Leu	Gly	Gly	Glu	Arg	Arg	Thr	Arg	Arg	Glu	Ser	Arg
				85					90					95	
Gln	Glu	Ser	Asp	Pro	Glu	Asp	Asp	Asp	Val	Lys	Lys	Pro	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Val	Val	Ala	Thr	Ser	Lys	Glu	Arg	Thr	Arg	Arg	Asp	Leu	Ile
		115					120					125			
Gln	Asp	Gln	Asn	Met	Asp	Glu	Lys	Gly	Lys	Gln	Arg	Asn	Arg	Arg	Ile
		130					135				140				
Phe	Gly	Leu	Leu	Met	Gly	Thr	Leu	Gln	Lys	Phe	Lys	Gln	Glu	Ser	Thr
145					150					155					160
Val	Ala	Thr	Glu	Arg	Gln	Asn	Arg	Arg	Gln	Glu	Ile	Glu	Gln	Lys	Leu
				165					170					175	
Glu	Val	Gln	Ala	Glu	Glu	Glu	Arg	Lys	Gln	Val	Glu	Asn	Glu	Arg	Arg
			180					185					190		
Glu	Leu	Phe	Glu	Glu	Arg	Arg	Ala	Lys	Gln	Thr	Glu	Leu	Arg	Leu	Leu
		195					200					205			
Glu	Gln	Lys	Val	Glu	Leu	Ala	Gln	Leu	Gln	Glu	Glu	Trp	Asn	Glu	His
		210				215					220				
Asn	Ala	Lys	Ile	Ile	Lys	Tyr	Ile	Arg	Thr	Lys	Thr	Lys	Pro	His	Leu
225					230					235					240
Phe	Tyr	Ile	Pro	Gly	Arg	Met	Cys	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Glu
				245					250					255	
Glu	Ser	Gln	Arg	Lys	Met	Asn	Ala	Leu	Phe	Asp	Gly	Arg	Arg	Ile	Glu
			260					265					270		
Phe	Ala	Glu	Gln	Ile	Asn	Lys	Met	Glu	Ala	Arg	Pro	Arg	Arg	Gln	Ser
		275					280					285			
Met	Lys	Glu	Lys	Glu	His	Gln	Val	Val	Arg	Asn	Glu	Glu	His	Lys	Ala
		290				295					300				
Glu	Gln	Glu	Glu	Gly	Lys	Val	Ala	Gln	Arg	Glu	Glu	Glu	Leu	Val	Glu
305				310						315					320
Thr	Gly	Asn	Gln	His	Asn	Asp	Val	Glu	Ile	Glu	Glu	Ala	Gly	Glu	Glu
				325					330					335	
Glu	Glu	Lys	Glu	Ile	Gly	Ile	Val	His	Ser	Asp	Ala	Glu	Lys	Glu	Gln
			340					345					350		
Glu	Glu	Glu	Glu	Gln	Lys	Gln	Glu	Met	Glu	Val	Lys	Met	Glu	Glu	Glu
		355					360					365			
Thr	Glu	Val	Arg	Glu	Ser	Glu	Lys	Gln	Gln	Asp	Ser	Gln	Pro	Glu	Glu
		370				375					380				
Val	Met	Asp	Val	Leu	Glu	Met	Val	Glu	Asn	Val	Lys	His	Val	Ile	Ala
385				390						395					400
Asp	Gln	Glu	Val	Met	Glu	Thr	Asn	Arg	Val	Glu	Ser	Val	Glu	Pro	Ser
				405					410					415	
Glu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Glu	Pro	Glu	Met	Glu	Phe	Glu	Ile
			420					425					430		
Glu	Pro	Asp	Lys	Glu	Cys	Lys	Ser	Leu	Ser	Pro	Gly	Lys	Glu	Asn	Val
		435					440					445			
Ser	Ala	Leu	Asp	Met	Glu	Lys	Glu	Ser	Asp	Glu	Lys	Glu	Glu	Lys	Glu
		450				455					460				
Ser	Glu	Pro	Gln	Pro	Glu	Pro	Val	Ala	Gln	Pro	Gln	Ala	Gln	Ser	Gln
465				470						475					480
Pro	Gln	Leu	Gln	Leu	Gln	Ser	Gln	Ser	Glu	Pro	Gln	Pro	Gln	Leu	Gln
				485					490					495	
Pro	Glu	Pro	Ala	Gln	Pro	Gln	Leu	Gln	Ser	Gln	Pro	Gln	Leu	Gln	Leu
			500					505					510		
Gln	Ser	Gln	Cys	His	Ala	Val	Leu	Gln	Ser	His	Pro	Pro	Ser	Gln	Pro
		515					520					525			
Glu	Asp	Leu	Ser	Leu	Ala	Val	Leu	Gln	Pro	Thr	Pro	Gln	Val	Thr	Gln

530		535		540
Glu His Gly His Phe Leu	Pro Glu Arg Lys Asp	Phe Pro Val Glu Ser		
545	550	555	560	
Val Lys Leu Thr Glu Val	Pro Val Asp Pro Val	Leu Thr Val His Pro		
	565	570	575	
Glu Ser Glu Ser Glu Thr	Asn Thr Arg Ser Arg	Ser Arg Gly Arg Thr		
	580	585	590	
Arg Asn Arg Thr Thr Lys	Ser Arg Ser Arg Ser	Ser Ser Ser Ser		
	595	600	605	
Ser Ser Ser Ser Ser Thr	Ser Ser Ser Ser Gly	Ser Ser Ser Ser		
	610	615	620	
Gly Ser Ser Ser Ser Arg	Ser Ser Ser Ser Ser	Ser Ser Ser Thr Ser		
625	630	635	640	
Gly Ser Ser Ser Arg Asp	Ser Ser Ser Ser Thr	Ser Ser Ser Ser Glu		
	645	650	655	
Ser Arg Ser Arg Ser Arg	Gly Arg Gly His Asn	Arg Asp Arg Lys His		
	660	665	670	
Arg Arg Ser Val Asp Arg	Lys Arg Arg Asp Thr	Ser Gly Leu Glu Arg		
	675	680	685	
Ser His Lys Ser Ser Lys	Gly Gly Ser Ser Arg	Asp Thr Lys Gly Ser		
	690	695	700	
Lys Asp Lys Asn Ser Arg	Ser Asp Arg Lys Arg	Ser Ile Ser Glu Ser		
705	710	715	720	
Ser Arg Ser Gly Lys Arg	Ser Ser Arg Ser Glu	Arg Asp Arg Lys Ser		
	725	730	735	
Asp Arg Lys Asp Lys Arg	Arg			
	740			

<210> 189
 <211> 1182
 <212> DNA
 <213> Homo sapiens

<400> 189
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 gccaggtaac aatgggtgcg ctgcaatcca gacagtaatt ctgcaaactg ccttgaagaa 180
 aaaggaccaa tggtcgaact acttccagggt gaatccaaca agatcccccg tctgaggact 240
 gacctttttc caaagacgag aatccaggac ttgaatcgta tottcccact ttctgaggac 300
 tactctggat caggcttcgg ctccggctcc ggctctggat caggatctgg gagtggcttc 360
 ctaacggaaa tggaacagga ttaccaacta gtagacgaaa gtgatgcttt ccatgacaac 420
 cttaggcttc ttgacaggaa tctgccctca gacagccagg acttgggtca acatggatta 480
 gaagaggatt ttatgttata aaagaggatt ttcccacctt gacaccaggc aatgtagtta 540
 gcatatttta tgtaccatgg ttatatgatt aatcttggga caaagaattt tatagaaatt 600
 tttaaacatc tgaaaaagaa gcttaagttt tatcatcctt ttttttctca tgaattctta 660
 aaggattatg ctttaatgct gttatctatc ttattgttct tgaaaatacc tgcatttttt 720
 ggtatcatgt tcaaccaaca tcattatgaa attaattaga ttcccatggc cataaaatgg 780
 ctttaaagaa tatatatata tttttaagt agcttgagaa gcaaattggc aggtaattat 840
 tcatacctaa attaagactc tgacttggat tgtgaattat aatgatatgc cccttttctt 900
 ataaaaacaa aaaaaaata atgaaacaca gtgaatttgt agagtggggg tatttgacat 960
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 gtattttcaa atgttactat atattaaagc agaaatataa cc 1182

<210> 190
 <211> 158
 <212> PRT

<213> Homo sapiens

<400> 190

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Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala
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Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg
           20           25           30
Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn
           35           40           45
Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser
 50           55           60
Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile
 65           70           75           80
Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser
           85           90           95
Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Phe
           100          105          110
Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala
           115          120          125
Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser
           130          135          140
Gln Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
145           150           155

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<210> 191

<211> 1595

<212> DNA

<213> Homo sapiens

<400> 191

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cgtgtaaaaca cactacttat cattgatgca tatataaaac cattttattt tcgctattat 180
ttcagaggaa gcgcctctga tttgtttcct ttttcccttt ttgctctttc tggctgtgtg 240
gtttggagaa agcacagttg gagtagccgg ttgctaaata agtcccagc gcgagcggag 300
acgatgcagc ggagactggt tcagcagtgg agcgtcgcgg tgttcctgct gagctacgcg 360
gtgccctcct gcgggcgctc ggtggagggt ctcagccgcc gcctcaaaag agctgtgtct 420
gaacatcagc tcctccatga caaggggaag tccatccaag atttacggcg acgattcttc 480
cttcaccatc tgatcgcaga aatccacaca gctgaaatca gagctacctc ggaggtgtcc 540
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gagggcagat acctaactca ggaaactaac aaggtggaga cgtacaaaga gcagccgctc 660
aagacacctg ggaagaaaaa gaaaggcaag cccgggaaac gcaaggagca ggaaaagaaa 720
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catcaatcct ttaccactct accaaataat ttcatattca agcttcagaa gctagtgacc 1140
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ggtttttctc atgtatcttt ttgttcattg gcaagatgaa ataatttttc taggggtaatg 1560
ccgtaggaaa aataaaaactt cacattttaa aaaaaa 1595

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<210> 192
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 192
 Met Gln Arg Arg Leu Val Gln Gln Trp Ser Val Ala Val Phe Leu Leu
 1 5 10 15
 Ser Tyr Ala Val Pro Ser Cys Gly Arg Ser Val Glu Gly Leu Ser Arg
 20 25 30
 Arg Leu Lys Arg Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly
 35 40 45
 Lys Ser Ile Gln Asp Leu Arg Arg Phe Phe Leu His His Leu Ile
 50 55 60
 Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr Ser Glu Val Ser Pro
 65 70 75 80
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly
 85 90 95
 Ser Asp Asp Glu Gly Arg Tyr Leu Thr Gln Glu Thr Asn Lys Val Glu
 100 105 110
 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Gly
 115 120 125
 Lys Pro Gly Lys Arg Lys Glu Gln Glu Lys Lys Lys Arg Arg Thr Arg
 130 135 140
 Ser Ala Trp Leu Asp Ser Gly Val Thr Gly Ser Gly Leu Glu Gly Asp
 145 150 155 160
 His Leu Ser Asp Thr Ser Thr Thr Ser Leu Glu Leu Asp Ser Arg
 165 170 175

<210> 193
 <211> 2657
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 2623, 2624, 2625, 2626, 2627, 2628, 2629
 <223> n = A,T,C or G

<400> 193
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 actccatctt cgtgctcctc acaggccctg cctccctgcc tgctaaggac acagggaagg 120
 ggggtcccccac ctgagtgctt gcctcccttc cctgtgcctg tgtacctggc agtcacagcc 180
 acctggcgctg tcccagaaac caaccggctg acctcatctc ctgcccggcc ccacctccat 240
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 agggcctgag ccgtcgagct gcacccacag caggctgcct ttggtgactc accgggtgaa 360
 cgggggcatt gcgagcatc ccctccctgg gtttggtcc tgcccacggg gctgacagta 420
 gaaatcacag gctgtgagac agctggagcc cagctctgct tgaacctatt ttaggtctct 480
 gatccccgct tcctctttag actcccctag agctcagcca gtgctcaacc tgaggctggg 540
 ggtctctgag gaagagttag ttggagctga ggggtctggg gctgtcccct gagagagggg 600
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 gccctggcc cagcagccgc agctcccaac cacaatatcc tttggggttt ggcctacgga 720
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 ggagggggca aagttttcag ggtgttgttt agaattggga gatgtccctt gtatcaccat 1020
 ggaccctcat gataattttg tttctttcac tttctactct gttgacaacc attgtctcct 1080

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cttatttttct tttcattttc tgtaactttt tcgttaaact ttagcttgca tttgtaacga 1140
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ttaacatccc taaaattttc cttacatgtt ttactagcca gatttttctt cctctcctga 2580
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ggcagggcatg caagctt 2657

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<210> 194

<211> 168

<212> PRT

<213> Homo sapiens

<400> 194

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Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
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Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
20          25          30
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
35          40          45
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50          55          60
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65          70          75          80
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85          90          95
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100          105          110
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
115          120          125
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
130          135          140
Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Lys Glu Gly
145          150          155          160
Lys Lys Gln Glu Lys Met Leu Asp
165

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<210> 195

<211> 2972

<212> DNA

<213> Homo sapiens

<400> 195

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gggtctgtgg	tacgcaagaa	cctgctatca	gactgctctg	tcgtctctac	ctccctagag	180
gacaagcagc	aggttccatc	tgaggacagt	atggagaagg	tgaaagtata	cttgagggtt	240
aggcccttgt	taccttcaga	gttgaacga	caggaagatc	agggttgtgt	ccgtattgag	300
aatgtggaga	cccttgttct	acaagcacc	aaggactcgt	ttgccctgaa	gagcaatgaa	360
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caaggccaac	ttcatccaac	acctgatctg	aagcccttgc	tctccaatga	ggtaatctgg	660
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cacctcaacc	agaactccag	ccgcagtcac	agcatcttct	caatcaggat	cctacacctt	1200
cagggggaag	gagatatagt	ccccaaagac	agcgagctgt	cactctgtga	tctggctggc	1260
tcagagcgct	gcaaagatca	gaagagtgg	gaacgggtga	aggaagcagg	aaacattaac	1320
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gatgaaactc	ttcatgtggc	caagttctca	gccattgtga	gccagcttgt	gcatgcccc	1560
cctatgcaac	tgggattccc	atccctgcac	tcgttcatca	aggaacatag	tcttcaggta	1620
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gacacccaaa	aggaactatt	ggaggaaatg	tatgaagaaa	aactaaatat	cctcaaggag	1920
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<210> 196

<211> 890

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gln	Gly	Ile	Leu	Ser	Pro	Pro	Ala	Gly	Leu	Leu	Ser	Asp	Asp	1	5	10	15
Asp	Val	Val	Val	Ser	Pro	Met	Phe	Glu	Ser	Thr	Ala	Ala	Asp	Leu	Gly	20	25	30	
Ser	Val	Val	Arg	Lys	Asn	Leu	Leu	Ser	Asp	Cys	Ser	Val	Val	Ser	Thr	35	40	45	
Ser	Leu	Glu	Asp	Lys	Gln	Gln	Val	Pro	Ser	Glu	Asp	Ser	Met	Glu	Lys	50	55	60	
Val	Lys	Val	Tyr	Leu	Arg	Val	Arg	Pro	Leu	Leu	Pro	Ser	Glu	Leu	Glu	65	70	75	80
Arg	Gln	Glu	Asp	Gln	Gly	Cys	Val	Arg	Ile	Glu	Asn	Val	Glu	Thr	Leu	85	90	95	
Val	Leu	Gln	Ala	Pro	Lys	Asp	Ser	Phe	Ala	Leu	Lys	Ser	Asn	Glu	Arg	100	105	110	
Gly	Ile	Gly	Gln	Ala	Thr	His	Arg	Phe	Thr	Phe	Ser	Gln	Ile	Phe	Gly	115	120	125	
Pro	Glu	Val	Gly	Gln	Ala	Ser	Phe	Phe	Asn	Leu	Thr	Val	Lys	Glu	Met	130	135	140	
Val	Lys	Asp	Val	Leu	Lys	Gly	Gln	Asn	Trp	Leu	Ile	Tyr	Thr	Tyr	Gly	145	150	155	160
Val	Thr	Asn	Ser	Gly	Lys	Thr	His	Thr	Ile	Gln	Gly	Thr	Ile	Lys	Asp	165	170	175	
Gly	Gly	Ile	Leu	Pro	Arg	Ser	Leu	Ala	Leu	Ile	Phe	Asn	Ser	Leu	Gln	180	185	190	
Gly	Gln	Leu	His	Pro	Thr	Pro	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Asn	Glu	195	200	205	
Val	Ile	Trp	Leu	Asp	Ser	Lys	Gln	Ile	Arg	Gln	Glu	Glu	Met	Lys	Lys	210	215	220	
Leu	Ser	Leu	Leu	Asn	Gly	Gly	Leu	Gln	Glu	Glu	Glu	Leu	Ser	Thr	Ser	225	230	235	240
Leu	Lys	Arg	Ser	Val	Tyr	Ile	Glu	Ser	Arg	Ile	Gly	Thr	Ser	Thr	Ser	245	250	255	
Phe	Asp	Ser	Gly	Ile	Ala	Gly	Leu	Ser	Ser	Ile	Ser	Gln	Cys	Thr	Ser	260	265	270	
Ser	Ser	Gln	Leu	Asp	Glu	Thr	Ser	His	Arg	Trp	Ala	Gln	Pro	Asp	Thr	275	280	285	
Ala	Pro	Leu	Pro	Val	Pro	Ala	Asn	Ile	Arg	Phe	Ser	Ile	Trp	Ile	Ser	290	295	300	
Phe	Phe	Glu	Ile	Tyr	Asn	Glu	Leu	Leu	Tyr	Asp	Leu	Leu	Glu	Pro	Pro	305	310	315	320
Ser	Gln	Gln	Arg	Lys	Arg	Gln	Thr	Leu	Arg	Leu	Cys	Glu	Asp	Gln	Asn	325	330	335	
Gly	Asn	Pro	Tyr	Val	Lys	Asp	Leu	Asn	Trp	Ile	His	Val	Gln	Asp	Ala	340	345	350	
Glu	Glu	Ala	Trp	Lys	Leu	Leu	Lys	Val	Gly	Arg	Lys	Asn	Gln	Ser	Phe	355	360	365	
Ala	Ser	Thr	His	Leu	Asn	Gln	Asn	Ser	Ser	Arg	Ser	His	Ser	Ile	Phe	370	375	380	
Ser	Ile	Arg	Ile	Leu	His	Leu	Gln	Gly	Glu	Gly	Asp	Ile	Val	Pro	Lys	385	390	395	400
Ile	Ser	Glu	Leu	Ser	Leu	Cys	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Cys	Lys	405	410	415	
Asp	Gln	Lys	Ser	Gly	Glu	Arg	Leu	Lys	Glu	Ala	Gly	Asn	Ile	Asn	Thr	420	425	430	
Ser	Leu	His	Thr	Leu	Gly	Arg	Cys	Ile	Ala	Ala	Leu	Arg	Gln	Asn	Gln	435	440	445	

Gln	Asn	Arg	Ser	Lys	Gln	Asn	Leu	Val	Pro	Phe	Arg	Asp	Ser	Lys	Leu
	450					455					460				
Thr	Arg	Val	Phe	Gln	Gly	Phe	Phe	Thr	Gly	Arg	Gly	Arg	Ser	Cys	Met
465					470					475					480
Ile	Val	Asn	Val	Asn	Pro	Cys	Ala	Ser	Thr	Tyr	Asp	Glu	Thr	Leu	His
				485					490					495	
Val	Ala	Lys	Phe	Ser	Ala	Ile	Ala	Ser	Gln	Leu	Val	His	Ala	Pro	Pro
				500				505					510		
Met	Gln	Leu	Gly	Phe	Pro	Ser	Leu	His	Ser	Phe	Ile	Lys	Glu	His	Ser
		515					520					525			
Leu	Gln	Val	Ser	Pro	Ser	Leu	Glu	Lys	Gly	Ala	Lys	Ala	Asp	Thr	Gly
	530					535					540				
Leu	Asp	Asp	Asp	Ile	Glu	Asn	Glu	Ala	Asp	Ile	Ser	Met	Tyr	Gly	Lys
545					550					555					560
Glu	Glu	Leu	Leu	Gln	Val	Val	Glu	Ala	Met	Lys	Thr	Leu	Leu	Leu	Lys
				565					570						575
Glu	Arg	Gln	Glu	Lys	Leu	Gln	Leu	Glu	Met	His	Leu	Arg	Asp	Glu	Ile
				580				585					590		
Cys	Asn	Glu	Met	Val	Glu	Gln	Met	Gln	Gln	Arg	Glu	Gln	Trp	Cys	Ser
	595						600					605			
Glu	His	Leu	Asp	Thr	Gln	Lys	Glu	Leu	Leu	Glu	Glu	Met	Tyr	Glu	Glu
	610					615					620				
Lys	Leu	Asn	Ile	Leu	Lys	Glu	Ser	Leu	Thr	Ser	Phe	Tyr	Gln	Glu	Glu
625					630					635					640
Ile	Gln	Glu	Arg	Asp	Glu	Lys	Ile	Glu	Glu	Leu	Glu	Ala	Leu	Leu	Gln
				645					650						655
Glu	Ala	Arg	Gln	Gln	Ser	Val	Ala	His	Gln	Gln	Ser	Gly	Ser	Glu	Leu
				660				665					670		
Ala	Leu	Arg	Arg	Ser	Gln	Arg	Leu	Ala	Ala	Ser	Ala	Ser	Thr	Gln	Gln
	675						680					685			
Leu	Gln	Glu	Val	Lys	Ala	Lys	Leu	Gln	Gln	Cys	Lys	Ala	Glu	Leu	Asn
	690					695					700				
Ser	Thr	Thr	Glu	Glu	Leu	His	Lys	Tyr	Gln	Lys	Met	Leu	Glu	Pro	Pro
705					710					715					720
Pro	Ser	Ala	Lys	Pro	Phe	Thr	Ile	Asp	Val	Asp	Lys	Lys	Leu	Glu	Glu
				725					730					735	
Gly	Gln	Lys	Asn	Ile	Arg	Leu	Leu	Arg	Thr	Glu	Leu	Gln	Lys	Leu	Gly
				740				745					750		
Glu	Ser	Leu	Gln	Ser	Ala	Glu	Arg	Ala	Cys	Cys	His	Ser	Thr	Gly	Ala
	755					760						765			
Gly	Lys	Leu	Arg	Gln	Ala	Leu	Thr	Thr	Cys	Asp	Asp	Ile	Leu	Ile	Lys
	770					775					780				
Gln	Asp	Gln	Thr	Leu	Ala	Glu	Leu	Gln	Asn	Asn	Met	Val	Leu	Val	Lys
785					790					795					800
Leu	Asp	Leu	Arg	Lys	Lys	Ala	Ala	Cys	Ile	Ala	Glu	Gln	Tyr	His	Thr
				805					810					815	
Val	Leu	Lys	Leu	Gln	Gly	Gln	Val	Ser	Ala	Lys	Lys	Arg	Leu	Gly	Thr
				820				825					830		
Asn	Gln	Glu	Asn	Gln	Gln	Pro	Asn	Gln	Gln	Pro	Pro	Gly	Lys	Lys	Pro
				835			840					845			
Phe	Leu	Arg	Asn	Leu	Leu	Pro	Arg	Thr	Pro	Thr	Cys	Gln	Ser	Ser	Thr
	850					855					860				
Asp	Cys	Ser	Pro	Tyr	Ala	Arg	Ile	Leu	Arg	Ser	Arg	Arg	Ser	Pro	Leu
865					870					875					880
Leu	Lys	Ser	Gly	Pro	Phe	Gly	Lys	Lys	Tyr						
				885					890						

<211> 768
 <212> DNA
 <213> Homo sapiens

<400> 197
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 ctatgagcac tgggcctgtg atataggaga tgggtacgtg atccatctgg ctctccaag 180
 tgagtacccc ggggctggct cctccagtgt cttctcagtc ctgagcaaca gtgcagaggt 240
 gaaacggggg cgcctggaag atgtggtggg aggctgttgc tatcggtca acaacagctt 300
 ggaccatgag taccaaccac ggcccgtgga ggtgatcatc agttctgcga aggagatggg 360
 tggtcagaag atgaagtaca gtattgtgag caggaactgt gagcactttg tcgccagct 420
 gagatatggc aagtcccgtg gtaaacaggt ggaaaaggcc aagggtgaag tcggtgtggc 480
 cacggcgctt ggaatcctgg ttgttgctgg atgctctttt gcgattagga gatacaaaa 540
 aaaagcaaca gcctgaagca gccacaaaat cctgtgttag aagcagctgt ggggggtcca 600
 gtggagatga gcctcccca tgccctcagc agcctgacct tcgtgccctg tctcaggcgt 660
 tctctagatc ctttcctctg tttccctctc tcgtggcaa aagtatgatc taattgaaac 720
 aagactgaag gatcaataaa cagccatctg ccccttcaaa aaaaaaaa 768

<210> 198
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 198
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 Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr
 20 25 30
 Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
 35 40 45
 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Gly Arg
 50 55 60
 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65 70 75 80
 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95
 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110
 Cys Glu His Phe Val Ala Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 115 120 125
 Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
 130 135 140
 Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys
 145 150 155 160
 Lys Ala Thr Ala

<210> 199
 <211> 720
 <212> DNA
 <213> Homo sapiens

<400> 199
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 gctgtcccg cagtctccag ccgtcccgcc cgcttgtggc caaactggct ccagtcactc 120
 ccgaaatgcc agtcgacttc actgggtact ggaagatgtt ggtcaacgag aatttcgagg 180
 agtacctgcg cgccctcgac gtcaatgtgg ccttgcgcaa aatcgccaac ttgctgaagc 240

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cagacaaaga gatcgtgcag gacggtgacc atatgatcat ccgcacgctg agcactttta 300
ggaactacat catggacttc caagttggga aggagtttga ggaggatctg acaggcatag 360
atgaccgcaa gtgcatgaca acagtgaact gggacggaga caagctccag tgtgtgcaga 420
agggtgagaa ggaggggctg ggctggaccc agtggatcga ggggtgatgag ctgcacctag 480
agatgagagt ggaaggtgtg gtctgcaagc aagtattcaa gaaggtgcag tgaggcccaa 540
gcagacaacc ttgtcccaac caatcagcag gatgtgtgag ccaggatccc tctttgcaca 600
gcatgaggca aaaatgtcca gccacccta ggcattctgtt agcagagtct gtctcttggc 660
tttgtcactt ttccttttct taaaacaaa ccatgccaat aaagtgcact gtgttcaaaa 720

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<210> 200

<211> 135

<212> PRT

<213> Homo sapiens

<400> 200

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Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
 1          5          10          15
Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
 20          25          30
Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
 35          40          45
His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
 50          55          60
Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
 65          70          75          80
Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
 85          90          95
Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
100          105          110
Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
115          120          125
Gln Val Phe Lys Lys Val Gln
130          135

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<210> 201

<211> 2383

<212> DNA

<213> Homo sapiens

<400> 201

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ccacctgcct ggagagagcc aaagagttca agacacgtct ggggatcttt cttcacaaat 180
cagagctggg ctgcgatact gggagtactg gcaagtcgga gtggggcagt aaacacagca 240
aagagaatag aaacttctca gaagatgtgc tgggggtggag agagtcgttc gacctgctgc 300
tgagcagtaa aaatggagtg gctgccttcc acgctttcct gaagacagag ttcagttagg 360
agaacctgga gttctggctg gcctgtgagg agttcaagaa gatccgatca gctaccaagc 420
tggcctccag ggcacaccag atctttgagg agttcatttg cagttaggcc cctaaagagg 480
tcaacattga ccatgagacc cgcgagctga cgaggatgaa cctgcagact gccacagcca 540
catgctttga tgcggtcag ggaagacac gtaccctgat ggagaaggac tcctaccac 600
gcttcctgaa gtgcctgct taccgggacc tggtgcccga agcctcagcc gcctctgcca 660
ctctgtccag ctgcagcctg gacgagccct cacacacctg agtctccacg gcagttagga 720
agccagccgg gaagagagg ttagtcaccc atccccgagg tggctgccc tgtgtgggag 780
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ctccagcagc ctgtttggga agcagcagtc tctccttcag atactgtggg actcatgctg 900
gagaggagcc gccacttcc aggacctgtg aataagggct aatgatgagg gttggtgggg 960
ctctctgtgg ggcaaaaagg tggatatggg gtttagcact gctctcgttc tcaccggaga 1020

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aggaagtgtt ctagtgttgt ttaggaaaca tgtggataaa gggaaaccatg aaaatgagag 1080
gaggaaagac atccagatca gctgttttgc ctgttgctca gttgactctg attgcatcct 1140
gttttcctaa ttcccagact gttctgggca cggaaggac cctggatgtg gagtcttccc 1200
ctttggccct cctcactggc ctctgggcta gccagagtc ccttagcttg tacctcgtaa 1260
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tcttcctgga tgtgccctct ctgagttctg tgctgtctct tggaggcagg gccaggaga 1560
acaaagtgtg gaggcctcgg ggagtggctt ttccagctct catgccccgc agtgtggaac 1620
aaggcagaaa aggatcctag gaaataagtc tcttggcggg ccctgagagt cctgctgaaa 1680
tccagccagt gttttttgtg gtatgagaac aggcaaaaag agatgccccg agatagaagg 1740
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caggaccatg gcaccttag agtgcagaag ctgggggggag aggctgcttc gaaggcgagg 1860
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tcttgccgca gagcccaggc tggggaagtg aactaccag gccagcccct ttgtggcca 1980
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gactgtctcc ctttctctac cagactctac ctctgaatgt gctgggaacc tcttgagacc 2220
tgtcaggaac tcctcactgt ttaaatattt atttattgtg acaaattggag ctggtttcct 2280
agatatgaat gatgtttgca atccccattt tcctgtttca gcatgttata ttcttataaa 2340
ataaaaycaa aagtcaaata tgaaaaaaa aaaaaaaaaa aaa 2383

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<210> 202

<211> 202

<212> PRT

<213> Homo sapiens

<400> 202

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Met Cys Arg Thr Leu Ala Ala Phe Pro Thr Thr Cys Leu Glu Arg Ala
 1          5          10          15
Lys Glu Phe Lys Thr Arg Leu Gly Ile Phe Leu His Lys Ser Glu Leu
 20          25          30
Gly Cys Asp Thr Gly Ser Thr Gly Lys Ser Glu Trp Gly Ser Lys His
 35          40          45
Ser Lys Glu Asn Arg Asn Phe Ser Glu Asp Val Leu Gly Trp Arg Glu
 50          55          60
Ser Phe Asp Leu Leu Leu Ser Ser Lys Asn Gly Val Ala Ala Phe His
 65          70          75          80
Ala Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Leu
 85          90          95
Ala Cys Glu Glu Phe Lys Lys Ile Arg Ser Ala Thr Lys Leu Ala Ser
100          105          110
Arg Ala His Gln Ile Phe Glu Glu Phe Ile Cys Ser Glu Ala Pro Lys
115          120          125
Glu Val Asn Ile Asp His Glu Thr Arg Glu Leu Thr Arg Met Asn Leu
130          135          140
Gln Thr Ala Thr Ala Thr Cys Phe Asp Ala Ala Gln Gly Lys Thr Arg
145          150          155          160
Thr Leu Met Glu Lys Asp Ser Tyr Pro Arg Phe Leu Lys Ser Pro Ala
165          170          175
Tyr Arg Asp Leu Ala Ala Gln Ala Ser Ala Ala Ser Ala Thr Leu Ser
180          185          190
Ser Cys Ser Leu Asp Glu Pro Ser His Thr
195          200

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<210> 203

<211> 616
 <212> DNA
 <213> Homo sapiens

<400> 203
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 gccacagatc catgatgtgc agttctctgg agcaggcgct ggctgtgctg gtcactacct 120
 tccacaagta ctctgcca gagggcgaca agttcaagct gagtaagggg gaaatgaagg 180
 aacttctgca caaggagctg cccagctttg tggggcattc cagagaacca tgtgctgtga 240
 gggccttccg agtccatctg ttaatacctg tcattggaga cttgagaaac cagagcccag 300
 aagggaagaa tgattgtccc aagatcacac agcactggag aaagtggatg aggaggggct 360
 gaagaagctg atgggcagcc tggatgagaa cagtgaccag cagggtggact tccaggagta 420
 tgctgttttc ctggcactca tcaactgtcat gtgcaatgac ttcttccagg gctgcccaga 480
 ccgaccctga agcagaactc ttgacttcct gccatggatc tcttggggcc aggactgttg 540
 atgcctttga gttttgtatt caataaactt tttttgtctg ttgaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaaaaa 616

<210> 204
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr
 1 5 10 15
 Phe His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys
 20 25 30
 Gly Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly
 35 40 45
 His Ser Arg Glu Pro Cys Ala Val Arg Ala Phe Arg Val His Leu Phe
 50 55 60
 Asn Pro Val Ile Gly Asp Leu Arg Asn Gln Ser Pro Glu Gly Lys Ser
 65 70 75 80
 Asp Cys Pro Lys Ile Thr Gln His Trp Arg Lys Trp Met Arg Arg Gly
 85 90 95

<210> 205
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 205
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 ggcgctggct gtgctggtca ctaccttcca caagtactcc tgccaagagg gcgacaagtt 120
 caagctgagt aagggggaaa tgaaggaact tctgcacaag gagctgcca gctttgtggg 180
 ggagaaagtg gatgaggagg ggctgaagaa gctgatgggc agcctggatg agaacagtga 240
 ccagcaggtg gacttccagg agtatgctgt tttcctggca ctcactactg tcatgtgcaa 300
 tgactttctc cagggtgcc cagaccgacc ctgaagcaga actcttgact tcctgccatg 360
 gatctcttgg gccaggact gttgatgcct ttgagttttg tattcaataa actttttttg 420
 tctgttga 428

<210> 206
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 206
 Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr Phe

270

1	5	10	15
His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys Gly			
	20	25	30
Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly Glu			
	35	40	45
Lys Val Asp Glu Glu Gly Leu Lys Lys Leu Met Gly Ser Leu Asp Glu			
	50	55	60
Asn Ser Asp Gln Gln Val Asp Phe Gln Glu Tyr Ala Val Phe Leu Ala			
65	70	75	80
Leu Ile Thr Val Met Cys Asn Asp Phe Phe Gln Gly Cys Pro Asp Arg			
	85	90	95
Pro			

<210> 207

<211> 799

<212> DNA

<213> Homo sapiens

<400> 207

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cactcccaaa gaactgggta ctcaacactg agcagatctg ttctttgagc taaaaaccat 60
gtgctgtacc aagagtttgc tcctggctgc tttgatgtca gtgctgtac tccacctctg 120
cggcgaatca gaagcagcaa gcaactttga ctgctgtctt ggatacacag accgtattct 180
tcatacctaaa tttattgtgg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa 240
tgctatcatc tttcacacaa agaaaaagt gtctgtgtgc gcaaatacaa aacagacttg 300
ggtgaaatat attgtgcgtc tcctcagtaa aaaagtcaag aacatgtaaa aactgtggct 360
tttctggaat ggaattggac atagcccaag aacagaaaga accttgctgg ggttggaggt. 420
ttcacttgca catcatggag ggtttagtgc ttatctaatt tgtgcctcac tggacttgtc 480
caattaatga agttgattca tattgcatca tagtttgctt tgtttaagca tcacattaaa 540
gttaaaactgt attttatgtt atttatagct gtaggttttc tgtgttttagc tatttaatac 600
taattttcca taagctatatt tggtttagtg caaagtataa aattatatatt gggggggaat 660
aagattatat ggactttctt gcaagcaaca agctattttt taaaaaaact atttaacatt 720
cttttgttta tattgttttg tctcctaaat tgttgtaatt gcattataaa ataagaaaaa 780
cattaataag acaaatatt

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<210> 208

<211> 96

<212> PRT

<213> Homo sapiens

<400> 208

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
1	5
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
	20
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
	35
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
	50
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
65	70
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
	85
	90
	95

<210> 209

<211> 2133

<212> DNA

<213> Homo sapiens

<400> 209

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gaagccctgc ctgatgagac agaggtggtg gaagaaactg tggcagaggt gactgaggta 180
tctgtgggag ctaatcctgt ccaggtggaa gtaggagaat ttgatgatgg tgcagaggaa 240
accgaagagg aggtggtggc ggaaaatccc tgccagaacc accactgcaa acacggcaag 300
gtgtgcgagc tggatgagaa caacaccccc atgtgcgtgt gccaggaccc caccagctgc 360
ccagccccc ttggcgagtt tgagaagggt tgcagcaatg acaacaagac cttcgactct 420
tcctgccact tctttgccac aaagtgcacc ctggagggca ccaagaaggg ccacaagctc 480
cacctggact acatcggggc ttgcaaatac atccccctt gcctggactc tgagctgacc 540
gaattccccc tgcgcatgcg ggactggctc aagaacgtcc tggtcaccct gtatgagagg 600
gatgaggaca acaaccttct gactgagaag cagaagctgc ggggtgaagaa gatccatgag 660
aatgagaagc gcctggaggc aggagaccac cccgtggagc tgctggcccc ggacttcgag 720
aagaactata acatgtacat cttccctgta cactggcagt tcggccagct ggaccagcac 780
ccattgacg ggtacctctc ccacaccgag ctggctccac tgcgtgctcc cctcatcccc 840
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gccctggatg agtgggcccg ctgcttcggc atcaagcaga aggatatcga caaggatctt 960
gtgatctaaa tccactcctt ccacagtacc ggattctctc tttaaccctc cccttcgtgt 1020
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catagattta agtgaatata ttaacggtgc taaaaatgaa aattctaacc caagacatga 1140
cattcttagc tgttaactta ctattaagc cttttccaca cgcattaata gtcccatttt 1200
tctcttgcca tttgtagctt tgcccattgt cttattggca catgggtgga caggatctg 1260
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acatttggat gattgtcata aggtttttag catgttcttc cttttcttca ccctccccct 1920
tgttcttcta ttaatcaaga gaaacttcaa agttaatggg atggtcggat ctcacaggct 1980
gagaactcgt tcacctcaa gcatttcag aaaaagctgc ttcttattaa tcatacaaac 2040
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ctgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2133

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<210> 210

<211> 303

<212> PRT

<213> Homo sapiens

<400> 210

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Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1           5           10          15
Ala Ala Pro Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
20          25          30
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
35          40          45
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
50          55          60
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
65          70          75          80
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
85          90          95
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys

```

100					105					110						
Ser	Asn	Asp	Asn	Lys	Thr	Phe	Asp	Ser	Ser	Cys	His	Phe	Phe	Ala	Thr	
115					120					125						
Lys	Cys	Thr	Leu	Glu	Gly	Thr	Lys	Lys	Gly	His	Lys	Leu	His	Leu	Asp	
130					135					140						
Tyr	Ile	Gly	Pro	Cys	Lys	Tyr	Ile	Pro	Pro	Cys	Leu	Asp	Ser	Glu	Leu	
145					150					155					160	
Thr	Glu	Phe	Pro	Leu	Arg	Met	Arg	Asp	Trp	Leu	Lys	Asn	Val	Leu	Val	
165					170					175						
Thr	Leu	Tyr	Glu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Thr	Glu	Lys	Gln	
180					185					190						
Lys	Leu	Arg	Val	Lys	Lys	Ile	His	Glu	Asn	Glu	Lys	Arg	Leu	Glu	Ala	
195					200					205						
Gly	Asp	His	Pro	Val	Glu	Leu	Leu	Ala	Arg	Asp	Phe	Glu	Lys	Asn	Tyr	
210					215					220						
Asn	Met	Tyr	Ile	Phe	Pro	Val	His	Trp	Gln	Phe	Gly	Gln	Leu	Asp	Gln	
225					230					235					240	
His	Pro	Ile	Asp	Gly	Tyr	Leu	Ser	His	Thr	Glu	Leu	Ala	Pro	Leu	Arg	
245					250					255						
Ala	Pro	Leu	Ile	Pro	Met	Glu	His	Cys	Thr	Thr	Arg	Phe	Phe	Glu	Thr	
260					265					270						
Cys	Asp	Leu	Asp	Asn	Asp	Lys	Tyr	Ile	Ala	Leu	Asp	Glu	Trp	Ala	Gly	
275					280					285						
Cys	Phe	Gly	Ile	Lys	Gln	Lys	Asp	Ile	Asp	Lys	Asp	Leu	Val	Ile		
290					295					300						

<210> 211

<211> 2228

<212> DNA

<213> Homo sapiens.

<400> 211

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cctactccta aagtgattgg tattgatctt ggcaccacct attgttctgt tgggggtggtt 180
tttcctggca caggaaaagt aaagggtgatt ccagatgaaa atgggcatat cagcatatccc 240
agcatgggtg cttttactga caatgatgta tatgtgggat atgaaagcgt agagctggca 300
gattcaaatc ctcaaaacac aatatatgat gccaaaagat tcataggcaa gatttttacc 360
gcagaagagt tggaggctga aattggcaga taccatttta aggtttttaa caaaaatgga 420
atggttgagt tttctgtgac aagtaatgag accatcacag tgtccccaga atatgttggc 480
tctcgactat tgttgaagt aaaggaaatg gcagaggcat atcttggaaat gccagttgcc 540
aatgctgtca tttctgtacc agcagaattt gatctaaaac agagaaattc aacaattgaa 600
gctgctaacc ttgcaggact gaagattttg aggttaataa atgaaccac agcagcagct 660
atggcctatg gtctccacaa ggctgacgtc ttccacgtct tggatgata cttgggcgga 720
ggaactctag atgtgtcttt actgaataaa caaggaggga tgtttctaac ccgagcaatg 780
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agacaagctg tggaaatggg caaattaaat ctgactcttc atcaatctgc tcagttgtca 960
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ttgaaagaag gccacctgga aaagactgag attgatgagg tgggttttagt tgggggctcc 1260
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aacttcaact gaattctgca gaaataatgg ttatttgtga acttgtctga tgatctcttc 1500
ccatttatca gattacctt tccacaaaag aaagtctcta aaatatcaca gatttaccta 1560

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gagggcaaca tttagatata ggaaaatttt acatagtgtt ttgtcttagg attagacgtg 1620
accagattga tcctgtttga ttttggagag atcctattct aacaaatact ctaaaatgat 1680
aaaattgagg tacaactctc ttaaaaagagt atggataact atattttctg gattctggag 1740
gttgataacc atatgcactt aacattatat tctataaaca ttaagtagtg ccagttatga 1800
gattcccagt tcttactaaa ttgtattagc aggagctggg aattacttgt attatcacat 1860
gtaactaata atttgaacta tacttgaagg accgtgttga tgtcagggtat ttacagtggg 1920
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atataacaaa tttacattca caaattcagt atcctgttaa gtgtcatatt cttgtaattct 2040
gcattctcca ggagttttat gtgtttaata gatgaattta ttttatttct aaagggtattc 2100
aaatgtttca gcacatata atagaaatag ccaattatat tctagtctct ttatgtcctg 2160
tacatcattc tctgcttggg tttccattat tctgtttggg tagagaataa aattggtaat 2220
tgcatttg                                     2228

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<210> 212

<211> 471

<212> PRT

<213> Homo sapiens

<400> 212

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Met Ala Arg Glu Met Thr Ile Leu Gly Ser Ala Val Leu Thr Leu Leu
 1           5           10           15
Leu Ala Gly Tyr Leu Ala Gln Gln Tyr Leu Pro Leu Pro Thr Pro Lys
 20           25           30
Val Ile Gly Ile Asp Leu Gly Thr Thr Tyr Cys Ser Val Gly Val Phe
 35           40           45
Phe Pro Gly Thr Gly Lys Val Lys Val Ile Pro Asp Glu Asn Gly His
 50           55           60
Ile Ser Ile Pro Ser Met Val Ser Phe Thr Asp Asn Asp Val Tyr Val
 65           70           75           80
Gly Tyr Glu Ser Val Glu Leu Ala Asp Ser Asn Pro Gln Asn Thr Ile
 85           90           95
Tyr Asp Ala Lys Arg Phe Ile Gly Lys Ile Phe Thr Ala Glu Glu Leu
100           105           110
Glu Ala Glu Ile Gly Arg Tyr Pro Phe Lys Val Leu Asn Lys Asn Gly
115           120           125
Met Val Glu Phe Ser Val Thr Ser Asn Glu Thr Ile Thr Val Ser Pro
130           135           140
Glu Tyr Val Gly Ser Arg Leu Leu Leu Lys Leu Lys Glu Met Ala Glu
145           150           155           160
Ala Tyr Leu Gly Met Pro Val Ala Asn Ala Val Ile Ser Val Pro Ala
165           170           175
Glu Phe Asp Leu Lys Gln Arg Asn Ser Thr Ile Glu Ala Ala Asn Leu
180           185           190
Ala Gly Leu Lys Ile Leu Arg Val Ile Asn Glu Pro Thr Ala Ala Ala
195           200           205
Met Ala Tyr Gly Leu His Lys Ala Asp Val Phe His Val Leu Val Ile
210           215           220
Asp Leu Gly Gly Gly Thr Leu Asp Val Ser Leu Leu Asn Lys Gln Gly
225           230           235           240
Gly Met Phe Leu Thr Arg Ala Met Ser Gly Asn Asn Lys Leu Gly Gly
245           250           255
Gln Asp Phe Asn Gln Arg Leu Leu Gln Tyr Leu Tyr Lys Gln Ile Tyr
260           265           270
Gln Thr Tyr Gly Phe Val Pro Ser Arg Lys Glu Glu Ile His Arg Leu
275           280           285
Arg Gln Ala Val Glu Met Val Lys Leu Asn Leu Thr Leu His Gln Ser
290           295           300
Ala Gln Leu Ser Val Leu Leu Thr Val Glu Glu Gln Asp Arg Lys Glu
305           310           315           320

```

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Pro His Ser Ser Asp Thr Glu Leu Pro Lys Asp Lys Leu Ser Ser Ala
          325          330          335
Asp Asp His Arg Val Asn Ser Gly Phe Gly Arg Gly Leu Ser Asp Lys
          340          345          350
Lys Ser Gly Glu Ser Gln Val Leu Phe Glu Thr Glu Ile Ser Arg Lys
          355          360          365
Leu Phe Asp Thr Leu Asn Glu Asp Leu Phe Gln Lys Ile Leu Val Pro
          370          375          380
Ile Gln Gln Val Leu Lys Glu Gly His Leu Glu Lys Thr Glu Ile Asp
385          390          395          400
Glu Val Val Leu Val Gly Gly Ser Thr Arg Ile Pro Arg Ile Arg Gln
          405          410          415
Val Ile Gln Glu Phe Phe Gly Lys Asp Pro Asn Thr Ser Val Asp Pro
          420          425          430
Asp Leu Ala Val Val Thr Gly Val Ala Ile Gln Ala Gly Ile Asp Gly
          435          440          445
Gly Ser Trp Pro Leu Gln Val Ser Ala Leu Glu Ile Pro Asn Lys His
          450          455          460
Leu Gln Lys Thr Asn Phe Asn
465          470

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<210> 213
 <211> 1224
 <212> DNA
 <213> Homo sapiens

<400> 213
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 agcaccctgc cccagcgagt cctccggaaa gagcctgtca ccccatctgc acttgtcctc 180
 atgagccgct ccaatgtcca gccacagct gccctggcc agaaggtgat ggagaatagc 240
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 cctctgggca aaggcaagtt tggaaacgtg tacttggtc gggagaagaa aagccatttc 360
 atcgtggcgc tcaaggtcct cttcaagtcc cagatagaga aggagggcgt ggagcatcag 420
 ctgcgcagag agatcgaaat ccaggcccac ctgcaccatc ccaacatcct gcgtctctac 480
 aactatTTTT atgaccggag gaggatctac ttgattctag agtatgcccc ccgcggggag 540
 ctctacaagg agctgcagaa gagctgcaca ttgacgagc agcgaacagc cacgatcatg 600
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 tatcgccgca tcgtcaaggt ggacctaaag ttccccgctt ctgtgcccac gggagcccag 960
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 tctgtgcct gatggtccct gtcattcact cgggtgcgtg tgtttgtatg tctgtgtatg 1140
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 ttaataaagg ctgaagcttt ttgt 1224

<210> 214
 <211> 344
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Ala Gln Lys Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln Thr
 1 5 10 15
 Ala Pro Ser Gly Leu Ser Thr Leu Pro Gln Arg Val Leu Arg Lys Glu

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<210> 215
<211> 1421
<212> DNA
<213> Homo sapiens
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<400> 215							
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agctgcatta	acctgccac	tgtgctgcc	ggctcccca	gcaagaccg	ggggcagatc	120	
cagtgattc	tcgggccgat	gttctcagga	aaaagcacag	agttgatgag	acgcgtccgt	180	
cgcttccaga	ttgctcagta	caagtgcctg	gtgatcaagt	atgccaaaga	cactcgctac	240	
agcagcagct	tctgcacaca	tgaccggaac	accatggagg	cgctgcccg	ctgcctgctc	300	
cgagacgtgg	cccaggaggc	cctgggcgtg	gctgtcatag	gcacgcagca	ggggcagttt	360	
ttccctgaca	tcatggagtt	ctgcgaggcc	atggccaacg	ccgggaagac	cgtaatttgt	420	
ctgacatcgg	atgggacctt	ccagaggaag	ccatttgggg	ccatcctgaa	cctgggtgcg	480	
gtggccgaga	gcgtggtgaa	gctgacggcg	gtgtgcatgg	agtgtctccg	ccgaagcgcc	540	
tataccaaga	ggctgggcac	agagaaggag	gtcgagggtga	ttggggggagc	agacaagtac	600	

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cactccgtgt gtcggctctg ctacttcaag aaggcctcag gccagcctgc cgggccggac 660
aacaagaga actgcccagt gccaggaaag ccaggggaag ccgtggctgc caggaagctc 720
tttgcacac agcagattct gcaatgcagc cctgccaact gagggacctg caagggccgc 780
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<210> 216

<211> 234

<212> PRT

<213> Homo sapiens

<400> 216

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Met Ser Cys Ile Asn Leu Pro Thr Val Leu Pro Gly Ser Pro Ser Lys
1           5           10           15
Thr Arg Gly Gln Ile Gln Val Ile Leu Gly Pro Met Phe Ser Gly Lys
20           25           30
Ser Thr Glu Leu Met Arg Arg Val Arg Arg Phe Gln Ile Ala Gln Tyr
35           40           45
Lys Cys Leu Val Ile Lys Tyr Ala Lys Asp Thr Arg Tyr Ser Ser Ser
50           55           60
Phe Cys Thr His Asp Arg Asn Thr Met Glu Ala Leu Pro Ala Cys Leu
65           70           75           80
Leu Arg Asp Val Ala Gln Glu Ala Leu Gly Val Ala Val Ile Gly Ile
85           90           95
Asp Glu Gly Gln Phe Phe Pro Asp Ile Met Glu Phe Cys Glu Ala Met
100          105          110
Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu Asp Gly Thr Phe
115          120          125
Gln Arg Lys Pro Phe Gly Ala Ile Leu Asn Leu Val Pro Leu Ala Glu
130          135          140
Ser Val Val Lys Leu Thr Ala Val Cys Met Glu Cys Phe Arg Glu Ala
145          150          155          160
Ala Tyr Thr Lys Arg Leu Gly Thr Glu Lys Glu Val Glu Val Ile Gly
165          170          175
Gly Ala Asp Lys Tyr His Ser Val Cys Arg Leu Cys Tyr Phe Lys Lys
180          185          190
Ala Ser Gly Gln Pro Ala Gly Pro Asp Asn Lys Glu Asn Cys Pro Val
195          200          205
Pro Gly Lys Pro Gly Glu Ala Val Ala Ala Arg Lys Leu Phe Ala Pro
210          215          220
Gln Gln Ile Leu Gln Cys Ser Pro Ala Asn
225          230

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<210> 217

<211> 2307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720, 1724, 1728,
1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791, 1802, 1821,
1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012, 2038, 2143

<223> n = A,T,C or G

<400> 217

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cctgccctgc actcgggcct cctccagcca gtgctgacca gggacttctg acctgctggc 180
cagccaggac ctgtgtgggg aggccctcct gctgccttgg ggtgacaatc tcagctccag 240
gctacaggga gaccgggagg atcacagagc cagcatgtta caggatcctg acagtgatca 300
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ccgatccaca ctgcagggtc tggactcggc cacagggaac tggttctctg cctgtttcga 660
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<210> 218

<211> 428

<212> PRT

<213> Homo sapiens

<400> 218

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      20             25             30
Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile
      35             40             45

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Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	Tyr	Phe	Leu	Cys
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Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	Leu	Cys	Asp	Gly	Glu
65				70					75						80
Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	His	Cys	Val	Lys	Ser	Phe
			85					90						95	
Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	Leu	Ser	Lys	Asp	Arg	Ser	Thr
			100					105					110		
Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe
		115					120					125			
Asp	Asn	Phe	Thr	Glu	Ala	Leu	Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly
	130				135					140					
Tyr	Ser	Ser	Lys	Pro	Thr	Phe	Arg	Ala	Val	Glu	Ile	Gly	Pro	Asp	Gln
145				150						155					160
Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	Ser	Gln	Glu	Leu	Arg	Met
			165					170						175	
Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	Gly	Ser	Leu	Val	Ser	Leu	His
			180				185						190		
Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	Lys	Thr	Pro	Arg	Val	Val	Gly	Gly
	195						200					205			
Glu	Glu	Ala	Ser	Val	Asp	Ser	Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr
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Asp	Lys	Gln	His	Val	Cys	Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val
225				230						235					240
Leu	Thr	Ala	Ala	His	Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp
			245					250						255	
Lys	Val	Arg	Ala	Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala
			260					265					270		
Val	Ala	Lys	Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp
		275					280					285			
Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly
	290				295						300				
Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
305				310						315					320
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	Gly
			325						330					335	
Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	Ile	Asp
			340					345					350		
Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	Val	Thr	Glu
		355				360						365			
Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	Asp	Thr	Cys	Gln
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Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	Asp	Gln	Trp	His	Val
385				390						395					400
Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	Gly	Gly	Pro	Ser	Thr	Pro
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<210> 219

<211> 556

<212> DNA

<213> Homo sapiens

<400> 219

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agtcgaaact gaagaagaca gagacgcaag agaaaaatcc actgccttcc aaagaaacga 180

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caaagagggt ggatcaagtt taaatgactg tgotgcccct ttcacatcaa agaactactg 360
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gaacttgcct gttggtgaag gaagaagtgg ggtggaagaa gtgggggtgg acgacagtga 480
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agtgccattt tttttt                                     556

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<210> 220

<211> 44

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ser Asp Lys Pro Asp Met Ala Glu Ile Glu Lys Phe Asp Lys Ser
 1             5             10             15
Lys Leu Lys Lys Thr Glu Thr Gln Glu Lys Asn Pro Leu Pro Ser Lys
             20             25             30
Glu Thr Ile Glu Gln Glu Lys Gln Ala Gly Glu Ser
             35             40

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<210> 221

<211> 4792

<212> DNA

<213> Homo sapiens

<400> 221

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tctgttgaaa gaatctatca aaagaaaaca caattggaac atattttgct ccgcccagac 180
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<210> 222

<211> 1531

<212> PRT

<213> Homo sapiens

<400> 222

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Ser	His	Lys	Gln	Ile	Met	Glu	Asn	Ala	Glu	Ile	Asn	Asn	Ile	Ile	Lys
			500					505					510		
Ile	Val	Gly	Leu	Gln	Tyr	Lys	Lys	Asn	Tyr	Glu	Asp	Glu	Asp	Ser	Leu
		515					520					525			
Lys	Thr	Leu	Arg	Tyr	Gly	Lys	Ile	Met	Ile	Met	Thr	Asp	Gln	Asp	Gln
		530				535					540				
Asp	Gly	Ser	His	Ile	Lys	Gly	Leu	Leu	Ile	Asn	Phe	Ile	His	His	Asn
545					550					555					560
Trp	Pro	Ser	Leu	Leu	Arg	His	Arg	Phe	Leu	Glu	Glu	Phe	Ile	Thr	Pro
			565						570					575	
Ile	Val	Lys	Val	Ser	Lys	Asn	Lys	Gln	Glu	Met	Ala	Phe	Tyr	Ser	Leu
			580					585					590		
Pro	Glu	Phe	Glu	Glu	Trp	Lys	Ser	Ser	Thr	Pro	Asn	His	Lys	Lys	Trp
		595					600					605			
Lys	Val	Lys	Tyr	Tyr	Lys	Gly	Leu	Gly	Thr	Ser	Thr	Ser	Lys	Glu	Ala
	610					615					620				
Lys	Glu	Tyr	Phe	Ala	Asp	Met	Lys	Arg	His	Arg	Ile	Gln	Phe	Lys	Tyr
625					630					635					640
Ser	Gly	Pro	Glu	Asp	Asp	Ala	Ala	Ile	Ser	Leu	Ala	Phe	Ser	Lys	Lys
				645					650					655	
Gln	Ile	Asp	Asp	Arg	Lys	Glu	Trp	Leu	Thr	Asn	Phe	Met	Glu	Asp	Arg
			660					665					670		
Arg	Gln	Arg	Lys	Leu	Leu	Gly	Leu	Pro	Glu	Asp	Tyr	Leu	Tyr	Gly	Gln
		675					680					685			
Thr	Thr	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	Leu	Ile
		690				695					700				
Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Met	Val	Asp
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Gly	Leu	Lys	Pro	Gly	Gln	Arg	Lys	Val	Leu	Phe	Thr	Cys	Phe	Lys	Arg
				725					730					735	
Asn	Asp	Lys	Arg	Glu	Val	Lys	Val	Ala	Gln	Leu	Ala	Gly	Ser	Val	Ala
			740					745					750		
Glu	Met	Ser	Ser	Tyr	His	His	Gly	Glu	Met	Ser	Leu	Met	Met	Thr	Ile
		755					760					765			
Ile	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Leu	Asn	Leu	Leu
	770					775					780				
Gln	Pro	Ile	Gly	Gln	Phe	Gly	Thr	Arg	Leu	His	Gly	Gly	Lys	Asp	Ser
785					790					795					800
Ala	Ser	Pro	Arg	Tyr	Ile	Phe	Thr	Met	Leu	Ser	Ser	Leu	Ala	Arg	Leu
				805					810					815	
Leu	Phe	Pro	Pro	Lys	Asp	Asp	His	Thr	Leu	Lys	Phe	Leu	Tyr	Asp	Asp
			820					825					830		
Asn	Gln	Arg	Val	Glu	Pro	Glu	Trp	Tyr	Ile	Pro	Ile	Ile	Pro	Met	Val
			835				840					845			
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	850					855					860				
Pro	Asn	Phe	Asp	Val	Arg	Glu	Ile	Val	Asn	Asn	Ile	Arg	Arg	Leu	Met
865					870					875					880
Asp	Gly	Glu	Glu	Pro	Leu	Pro	Met	Leu	Pro	Ser	Tyr	Lys	Asn	Phe	Lys
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Gly	Thr	Ile	Glu	Glu	Leu	Ala	Pro	Asn	Gln	Tyr	Val	Ile	Ser	Gly	Glu
			900					905					910		
Val	Ala	Ile	Leu	Asn	Ser	Thr	Thr	Ile	Glu	Ile	Ser	Glu	Leu	Pro	Val
		915					920					925			
Arg	Thr	Trp	Thr	Gln	Thr	Tyr	Lys	Glu	Gln	Val	Leu	Glu	Pro	Met	Leu
	930					935					940				
Asn	Gly	Thr	Glu	Lys	Thr	Pro	Pro	Leu	Ile	Thr	Asp	Tyr	Arg	Glu	Tyr
945					950					955					960
His	Thr	Asp	Thr	Thr	Val	Lys	Phe	Val	Val	Lys	Met	Thr	Glu	Glu	Lys

Thr Lys Arg Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro Asp
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 Pro Ala Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser Asp
 1460 1465 1470
 Asp Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr Ser
 1475 1480 1485
 Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp Ser
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 1505 1510 1515 1520
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<210> 223

<211> 1111

<212> DNA

<213> Homo sapiens

<400> 223

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<210> 224

<211> 284

<212> PRT

<213> Homo sapiens

<400> 224

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
 1 5 10 15
 Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
 20 25 30
 Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
 35 40 45
 Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
 50 55 60
 Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
 65 70 75 80
 Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
 85 90 95
 Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys

100	105	110
Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys		
115	120	125
Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln		
130	135	140
Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg		
145	150	155
Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu		
165	170	175
Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu		
180	185	190
Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu		
195	200	205
Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu		
210	215	220
Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu		
225	230	235
Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu		
245	250	255
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu		
260	265	270
Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile		
275	280	

<210> 225

<211> 501

<212> DNA

<213> Homo sapiens

<400> 225

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gaattcgctt tggatccatt tccatcggtc cttacagccg ctcgtcagac tccagcagcc 60
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gataaacttg tagtagttga cttctcagcc acgtggtgtg ggccttgcaa aatgatcaac 180
cctttctttc attccctctc tgaaaagtat tccaacgtga tattccttga agtagatgtg 240
gatgactgtc aggtgtgtgc ttcagagtgt gaagtcaaat gcacgccaac attccagttt 300
tttaagaagg gacaaaaggt ggggtgaattt tctggagcca ataaggaaaa gcttgaagcc 360
accattaatg aattagtcta atcatgtttt ctgaaaacat aaccagccat tggctattta 420
aacttgattt tttttattta caaaatataa atatgaagac ataaccagtt gccatctgcy 480
tgacaataaa cattatgcta a                                     501

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<210> 226

<211> 105

<212> PRT

<213> Homo sapiens

<400> 226

Met Val Lys Gln Ile Glu Ser Lys Thr Ala Phe Gln Glu Ala Leu Asp	
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Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys	
20	25
Gly Pro Cys Lys Met Ile Asn Pro Phe Phe His Ser Leu Ser Glu Lys	
35	40
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp	
50	55
Val Ala Ser Glu Cys Glu Val Lys Cys Thr Pro Thr Phe Gln Phe Phe	
65	70
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys	
85	90
	95

Leu Glu Ala Thr Ile Asn Glu Leu Val
100 105

<210> 227
<211> 783
<212> DNA
<213> Homo sapiens

<400> 227
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cccagccgcc actagcgtcg ccgcccgcgc taaaggagct gagccgagcg ggggcgccgc 120
ccgggggtccg gtggggcaaaa ggctacagca ggagctgatg accctcatga tgtctggcga 180
taaagggatt tctgccttcc ctgaatcaga caaccttttc aaatgggtag ggaccatcca 240
tggagcagct ggaacagtat atgaagacct gaggtataag ctctcgctag agttccccag 300
tggctaccct tacaatgcgc ccacagtga gttcctcacg ccctgctatc accccaacgt 360
ggacacccag ggtaacatat gcctggacat cctgaaggaa aagtgggtctg ccctgtatga 420
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cttgtgtcgt ctttttaatt tttccttaga tgggtctgtcc tttttgtgat ttctgtatag 660
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aaa 783

<210> 228
<211> 179
<212> PRT
<213> Homo sapiens

<400> 228
Met Ala Ser Gln Asn Arg Asp Pro Ala Ala Thr Ser Val Ala Ala Ala
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Arg Lys Gly Ala Glu Pro Ser Gly Gly Ala Ala Arg Gly Pro Val Gly
20 25 30
Lys Arg Leu Gln Gln Glu Leu Met Thr Leu Met Met Ser Gly Asp Lys
35 40 45
Gly Ile Ser Ala Phe Pro Glu Ser Asp Asn Leu Phe Lys Trp Val Gly
50 55 60
Thr Ile His Gly Ala Ala Gly Thr Val Tyr Glu Asp Leu Arg Tyr Lys
65 70 75 80
Leu Ser Leu Glu Phe Pro Ser Gly Tyr Pro Tyr Asn Ala Pro Thr Val
85 90 95
Lys Phe Leu Thr Pro Cys Tyr His Pro Asn Val Asp Thr Gln Gly Asn
100 105 110
Ile Cys Leu Asp Ile Leu Lys Glu Lys Trp Ser Ala Leu Tyr Asp Val
115 120 125
Arg Thr Ile Leu Leu Ser Ile Gln Ser Leu Leu Gly Glu Pro Asn Ile
130 135 140
Asp Ser Pro Leu Asn Thr His Ala Ala Glu Leu Trp Lys Asn Pro Thr
145 150 155 160
Ala Phe Lys Lys Tyr Leu Gln Glu Thr Tyr Ser Lys Gln Val Thr Ser
165 170 175
Gln Glu Pro

<210> 229
<211> 777

<212> DNA

<213> Homo sapiens

<400> 229

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gaacatgtcc ggtctaagac caaggttcct gtgcaggacc aggttctttt gctgggctcc 180
aagatcttaa agccacggag aagcctctca tcttatggca ttgacaaaga gaagaccatc 240
caccttacc tgaaagtggg gaagcccagt gatgaggagc tgcccttggt tcttgtggag 300
tcaggtgatg aggcaaagag gcacctcctc caggtgogaa ggtccagctc agtggcacia 360
gtgaaagcaa tgatcgagac taagacgggt ataatccctg agaccagat tgtgacttgc 420
aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggcaac 480
ttactcttcc tggcatctta ttgtattgga ggggtgaccac cctgggggatg ggggtgttggc 540
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tcccaaaatt aatgagaatg agatgagtag agtaagattt ggggtgggatg ggtaggatga 660
agtatattgc ccaactctat gtttctttga ttctaacaca attaattaag tgacatgatt 720
tttactaatg tattactgag actagtaaat aaatttttaa ggcaaaatag agcattc 777

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<210> 230

<211> 165

<212> PRT

<213> Homo sapiens

<400> 230

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Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
1          5          10          15
Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
20        25        30
Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
35        40        45
Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
50        55        60
Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65        70        75        80
Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
85        90        95
Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
100       105       110
Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
115       120       125
Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
130       135       140
Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145       150       155       160
Tyr Cys Ile Gly Gly
165

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<210> 231

<211> 4797

<212> DNA

<213> Homo sapiens

<400> 231

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ttctacaagc agtatccaag gggccgtgta tgttcaggga tgtttccata gacttctctc 180
aagaggaatg ggaatgcctg gacgctgatc agatgaattt atacaaagaa gtgatgttgg 240
agaatttcag caacctgggt tcagtgggac ttccaattc taagccagct gtgatctcct 300

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aagtaataat	taccctgtgaa	gacatgtcta	cttttattca	gcccacattt	cttattocac	480
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catatgcaac	tcaatacatg	attcatcaca	tacacagaat	taaaaataag	ccaggcactc	3780
acacctgtaa	tcccagcact	ttgcaaggcc	aaggcgggca	gatcacatga	tgtcaagagt	3840


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<210> 232

<211> 433

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 433

<223> Xaa = Any Amino Acid

<400> 232

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20 25 30
Gly Pro Val Met Phe Arg Asp Val Ser Ile Asp Phe Ser Gln Glu Glu
35 40 45
Trp Glu Cys Leu Asp Ala Asp Gln Met Asn Leu Tyr Lys Glu Val Met
50 55 60
Leu Glu Asn Phe Ser Asn Leu Val Ser Val Gly Leu Ser Asn Ser Lys
65 70 75 80
Pro Ala Val Ile Ser Leu Leu Glu Gln Gly Lys Glu Pro Trp Met Val
85 90 95
Asp Arg Glu Leu Thr Arg Gly Leu Cys Ser Asp Leu Glu Ser Met Cys
100 105 110
Glu Thr Lys Ile Leu Ser Leu Lys Lys Arg His Phe Ser Gln Val Ile
115 120 125
Ile Thr Arg Glu Asp Met Ser Thr Phe Ile Gln Pro Thr Phe Leu Ile
130 135 140
Pro Pro Gln Lys Thr Met Ser Glu Glu Lys Pro Trp Glu Cys Lys Ile
145 150 155 160
Cys Gly Lys Thr Phe Asn Gln Asn Ser Gln Phe Ile Gln His Gln Arg
165 170 175
Ile His Phe Gly Glu Lys His Tyr Glu Ser Lys Glu Tyr Gly Lys Ser
180 185 190
Phe Ser Arg Gly Ser Leu Val Thr Arg His Gln Arg Ile His Thr Gly
195 200 205
Lys Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Cys Ser
210 215 220
Ser Tyr Phe Ser Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
225 230 235 240
Glu Cys Lys Glu Cys Gly Lys Ala Phe Lys Tyr Cys Ser Asn Leu Asn

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Asp	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Val											
										260			265				270									
Cys	Gly	Lys	Ala	Phe	Thr	Lys	Ser	Ser	Gln	Leu	Phe	Leu	His	Leu	Arg											
										275			280				285									
Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala											
										290			295				300									
Phe	Thr	Gln	His	Ser	Arg	Leu	Ile	Gln	His	Gln	Arg	Met	His	Thr	Gly											
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Glu	Lys	Pro	Tyr	Glu	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Asn	Ser	Ala											
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Ser	Thr	Leu	Thr	Asn	His	His	Arg	Ile	His	Ala	Gly	Glu	Lys	Leu	Tyr											
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Glu	Cys	Glu	Glu	Cys	Arg	Lys	Ala	Phe	Ile	Gln	Ser	Ser	Glu	Leu	Ile											
										355			360				365									
Gln	His	Gln	Arg	Ile	His	Thr	Asp	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Glu											
										370			375				380									
Cys	Gly	Lys	Ala	Phe	Asn	Lys	Gly	Ser	Asn	Leu	Thr	Arg	His	Gln	Arg											
										385			390				395			400						
Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Asp	Cys	Lys	Glu	Cys	Gly	Lys	Ala											
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Xaa

<210> 233

<211> 1860

<212> DNA

<213> Homo sapiens

<400> 233

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gacccagag	tggaatgaag	ccactcacag	agggcatgag	gaagaatggc	acctggctgc	1380
aggctacagc	agccaccaca	cgtgactgtg	gcgtgaaccc	agaagaagca	gactcagcct	1440
tcagcctcct	ggccacctgc	tccttctatg	accatgcgct	ccacctctgg	gagtgggagg	1500
ggaactgagc	ttgaaatcat	gaagcccctt	cccacaagga	aaccaggagg	gagactgcga	1560

gtgagtgcc gggaccacct catcagagat gcttactgca gccctgcagg tgcctgggca 1620
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 ctggggccctt gaaagtggac tgggtgattc tgtctggcag agagtgggga aaagacgcgg 1740
 tttccagctt gcagatttgt taagttttctc aggcagattt tgacttttcag cctttcatac 1800
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<210> 234

<211> 501

<212> PRT

<213> Homo sapiens

<400> 234

Asp	Pro	Arg	Val	Arg	Ala	Arg	Ala	Asp	Gly	Val	Pro	Gly	Ala	Leu	Arg
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Ser	Ser	Gly	Arg	Pro	Arg	Pro	Arg	Arg	Pro	Ala	Gln	Tyr	Pro	Ala	Arg
			20					25					30		
Pro	Arg	Arg	Pro	Ala	Ser	Thr	Ala	Gly	Ser	Ala	Pro	Phe	Pro	Glu	Gly
			35				40					45			
Trp	Met	Met	Gly	Cys	Phe	Ala	Leu	Gln	Thr	Val	Asp	Thr	Glu	Leu	Thr
50						55					60				
Ala	Asp	Ser	Val	Glu	Trp	Cys	Pro	Leu	Gln	Gly	Cys	Arg	His	Leu	Leu
65					70					75				80	
Ala	Cys	Gly	Thr	Tyr	Gln	Leu	Arg	Arg	Pro	Glu	Asp	Arg	Pro	Ala	Gly
				85					90					95	
Pro	Gln	Asn	Lys	Gly	Gly	Met	Glu	Val	Lys	Glu	Pro	Gln	Val	Arg	Leu
			100					105					110		
Gly	Arg	Leu	Phe	Leu	Tyr	Ser	Phe	Asn	Asp	Asn	Asn	Ser	Ile	His	Pro
		115					120					125			
Leu	Val	Glu	Val	Gln	Arg	Lys	Asp	Thr	Ser	Ala	Ile	Leu	Asp	Met	Lys
130						135					140				
Trp	Cys	His	Ile	Pro	Val	Ala	Gly	His	Ala	Leu	Leu	Gly	Leu	Ala	Asp
145					150					155					160
Ala	Ser	Gly	Ser	Ile	Gln	Leu	Leu	Arg	Leu	Val	Glu	Ser	Glu	Lys	Ser
				165					170					175	
His	Val	Leu	Glu	Pro	Leu	Ser	Ser	Leu	Ala	Leu	Glu	Glu	Gln	Cys	Leu
			180					185					190		
Ala	Leu	Ser	Leu	Asp	Trp	Ser	Thr	Gly	Lys	Thr	Gly	Arg	Ala	Gly	Asp
			195				200					205			
Gln	Pro	Leu	Lys	Ile	Ile	Ser	Ser	Asp	Ser	Thr	Gly	Gln	Leu	His	Leu
210						215					220				
Leu	Met	Val	Asn	Glu	Thr	Arg	Pro	Arg	Leu	Gln	Lys	Val	Ala	Ser	Trp
225					230					235					240
Gln	Ala	His	Gln	Phe	Glu	Ala	Trp	Ile	Ala	Ala	Phe	Asn	Tyr	Trp	His
				245					250					255	
Pro	Glu	Ile	Val	Tyr	Ser	Gly	Gly	Asp	Asp	Gly	Leu	Leu	Arg	Gly	Trp
			260					265					270		
Asp	Thr	Arg	Val	Pro	Gly	Lys	Phe	Leu	Phe	Thr	Ser	Lys	Arg	His	Thr
			275				280					285			
Met	Gly	Val	Cys	Ser	Ile	Gln	Ser	Ser	Pro	His	Arg	Glu	His	Ile	Leu
290						295					300				
Ala	Thr	Gly	Ser	Tyr	Asp	Glu	His	Ile	Leu	Leu	Trp	Asp	Thr	Arg	Asn
305					310					315					320
Met	Lys	Gln	Pro	Leu	Ala	Asp	Thr	Pro	Val	Gln	Gly	Gly	Val	Trp	Arg
				325					330					335	
Ile	Lys	Trp	His	Pro	Phe	His	His	His	Leu	Leu	Leu	Ala	Ala	Cys	Met
			340					345					350		
His	Ser	Gly	Phe	Lys	Ile	Leu	Asn	Cys	Gln	Lys	Ala	Met	Glu	Glu	Arg
			355				360					365			

Gln Glu Ala Thr Val Leu Thr Ser His Thr Leu Pro Asp Ser Leu Val
 370 375 380
 Tyr Gly Ala Asp Trp Ser Trp Leu Leu Phe Arg Ser Leu Gln Arg Ala
 385 390 395 400
 Pro Ser Trp Ser Phe Pro Ser Asn Leu Gly Thr Lys Thr Ala Asp Leu
 405 410 415
 Lys Gly Ala Ser Glu Leu Pro Thr Pro Cys His Glu Cys Arg Glu Asp
 420 425 430
 Asn Asp Gly Glu Gly His Ala Arg Pro Gln Ser Gly Met Lys Pro Leu
 435 440 445
 Thr Glu Gly Met Arg Lys Asn Gly Thr Trp Leu Gln Ala Thr Ala Ala
 450 455 460
 Thr Thr Arg Asp Cys Gly Val Asn Pro Glu Glu Ala Asp Ser Ala Phe
 465 470 475 480
 Ser Leu Leu Ala Thr Cys Ser Phe Tyr Asp His Ala Leu His Leu Trp
 485 490 495
 Glu Trp Glu Gly Asn
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<210> 235

<211> 1614

<212> DNA

<213> Homo sapiens

<400> 235

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 ctcggttgcc cggccgggga cccgagccga aaagtatcgc tcagaatgtc gggcaaagac 180
 cgaattgaaa tctttccctc gcgaatggca cagaccatca tgaaggctcg tttaaaggga 240
 gcacagacag gtcgaaacct cctgaagaaa aaatctgatg ccttaactct tcgatttcga 300
 cagatcctaa agaagataat agagactaaa atgttgatgg gcgaagtgat gagagaagct 360
 gccttttcac tagctgaagc caagttcaca gcaggtgact tcagcactac agttatccaa 420
 aatgtcaata aagcgcaagt gaagattcga gcgaagaaag ataattgtagc aggtgttact 480
 ttgccagtat ttgaacatta ccatgaagga actgacagtt atgaactgac tggtttagcc 540
 agaggtgggg aacagttggc taaattaaag aggaattatg ccaaagcagt ggaactactg 600
 gtggaactag cttctctgca gacttctttt gttactttgg atgaagctat taagataacc 660
 aacaggcgtg taaatgccat tgaacatgtc atcattcccc ggattgaacg tactcttgct 720
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 caagagaaga aaaagattct aaaggaaaaa tctgagaagg acttgagaca aaggagagca 840
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 tttgaataat ctttctgtt ctggttcttt gagaaaccct aacactggct tcattttaat 960
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 ttgtaaaatt tacctagatg tctatttatg ggattacttt tgcagaatca taatttagca 1080
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 taaaatgatt taaaagtaag tcattccgtt tttattaatt tactgttaag tcatgttctc 1500
 atgctcagat cagtagtgct agccagagct ttctctgcag acatgtagga agtgggtagc 1560
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<210> 236

<211> 247

<212> PRT

<213> Homo sapiens

<400> 236

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Thr Ile Met Lys Ala Arg Leu Lys Gly Ala Gln Thr Gly Arg Asn Leu
      20           25           30
Leu Lys Lys Lys Ser Asp Ala Leu Thr Leu Arg Phe Arg Gln Ile Leu
      35           40           45
Lys Lys Ile Ile Glu Thr Lys Met Leu Met Gly Glu Val Met Arg Glu
      50           55           60
Ala Ala Phe Ser Leu Ala Glu Ala Lys Phe Thr Ala Gly Asp Phe Ser
65           70           75           80
Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val Lys Ile Arg Ala
      85           90           95
Lys Lys Asp Asn Val Ala Gly Val Thr Leu Pro Val Phe Glu His Tyr
      100          105          110
His Glu Gly Thr Asp Ser Tyr Glu Leu Thr Gly Leu Ala Arg Gly Gly
      115          120          125
Glu Gln Leu Ala Lys Leu Lys Arg Asn Tyr Ala Lys Ala Val Glu Leu
      130          135          140
Leu Val Glu Leu Ala Ser Leu Gln Thr Ser Phe Val Thr Leu Asp Glu
145          150          155          160
Ala Ile Lys Ile Thr Asn Arg Arg Val Asn Ala Ile Glu His Val Ile
      165          170          175
Ile Pro Arg Ile Glu Arg Thr Leu Ala Tyr Ile Ile Thr Glu Leu Asp
      180          185          190
Glu Arg Glu Arg Glu Glu Phe Tyr Arg Leu Lys Lys Ile Gln Glu Lys
      195          200          205
Lys Lys Ile Leu Lys Glu Lys Ser Glu Lys Asp Leu Glu Gln Arg Arg
      210          215          220
Ala Ala Gly Glu Val Leu Glu Pro Ala Asn Leu Leu Ala Glu Glu Lys
225          230          235          240
Asp Glu Asp Leu Leu Phe Glu
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<210> 237

<211> 1658

<212> DNA

<213> Homo sapiens

<400> 237

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gaactgccag ccaagatcct ggttgagttt gtggtggact ctcagaagaa agacaagctg 180
ctctgcagcc agcttcaggt agcggatttc ctgcagaaca tcctggctca ggaggacact 240
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aaggaacaat ggaaagagct gaaggccacc tacaggggagc acgtagaggc catcaaaatt 360
ggcctcacca aggccttgac tcagatggag gaagcccaga ggaaacggac acaactccgg 420
gaagcctttg agcagctcca ggccaagaaa caaatggcca tggagaaaacg cagagcagtc 480
cagaaccagt ggcagctaca acaggagaag catctgcagc atctggcgga ggtttctgca 540
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ggaaacctga agcagcaggc agaacaggag cgggacaagc tgcagaggta tcagaccttc 660
ctccagcttc tgtataccct gcagggtaag ctgttgttcc ctgaggctga ggctgaggca 720
gagaatcttc cagatgataa accccagcag ccgactcgac cccaggagca gactacagga 780
gacaccatgg ggagagacc ttgtgtgtcc ttcaaggctg ttggtctaca acctgctgga 840
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cctctgactt cctcacctc ccaaccatca ttacaggaaa gactgtgaac tcctgagttc 960
agcttgattt ctgactacat ccagcaagc tctggcatct gtggattaaa atccctggat 1020
ctctctcagt tgtgtatttg ttcattctca tatgctggca ggaacaacta ttaatacaga 1080

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tactcagaag ccaataacat gacaggagct gggactgggt tgaacacagg gtgtgcagat 1140
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ctagtgatac cttgatcttt cccactttct gttttcggat tggagaagat gtaccttttt 1560
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caaataaata ttttaaggta aaaaaaaaaa aaaaaaaaaa 1658

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<210> 238

<211> 277

<212> PRT

<213> Homo sapiens

<400> 238

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  20          25          30
Glu Leu Pro Ala Lys Ile Leu Val Glu Phe Val Val Asp Ser Gln Lys
  45          40          45
Lys Asp Lys Leu Leu Cys Ser Gln Leu Gln Val Ala Asp Phe Leu Gln
  50          55          60
Asn Ile Leu Ala Gln Glu Asp Thr Ala Lys Gly Leu Asp Pro Leu Ala
  65          70          75          80
Ser Glu Asp Thr Ser Arg Gln Lys Ala Ile Ala Ala Lys Glu Gln Trp
  85          90          95
Lys Glu Leu Lys Ala Thr Tyr Arg Glu His Val Glu Ala Ile Lys Ile
  100          105          110
Gly Leu Thr Lys Ala Leu Thr Gln Met Glu Glu Ala Gln Arg Lys Arg
  115          120          125
Thr Gln Leu Arg Glu Ala Phe Glu Gln Leu Gln Ala Lys Lys Gln Met
  130          135          140
Ala Met Glu Lys Arg Arg Ala Val Gln Asn Gln Trp Gln Leu Gln Gln
  145          150          155          160
Glu Lys His Leu Gln His Leu Ala Glu Val Ser Ala Glu Val Arg Glu
  165          170          175
Arg Lys Thr Gly Thr Gln Gln Glu Leu Asp Gly Val Phe Gln Lys Leu
  180          185          190
Gly Asn Leu Lys Gln Gln Ala Glu Gln Glu Arg Asp Lys Leu Gln Arg
  195          200          205
Tyr Gln Thr Phe Leu Gln Leu Leu Tyr Thr Leu Gln Gly Lys Leu Leu
  210          215          220
Phe Pro Glu Ala Glu Ala Glu Ala Glu Asn Leu Pro Asp Asp Lys Pro
  225          230          235          240
Gln Gln Pro Thr Arg Pro Gln Glu Gln Ser Thr Gly Asp Thr Met Gly
  245          250          255
Arg Asp Pro Gly Val Ser Phe Lys Ala Val Gly Leu Gln Pro Ala Gly
  260          265          270
Asp Val Asn Leu Pro
  275

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